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“Examiner Search Notes”

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James Martinell
Primary Examiner 1631

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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 17:02:55 ; Search time 106 Seconds
(without alignments)
6891.406 Million cell updates/sec

Title: US-09-700-696c-1
Perfect score: 1655
Sequence: 1 gtgaataaagaatataatgttat.....ataaaaaaaaaaaaaaa 1655

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5 summaries

Database : Issued_Patents_NA:*

1: /cgn2_5/ptodata/1/ina/5A_COMB_seq:
2: /cgn2_6/ptodata/1/ina/5B_COMB_seq:
3: /cgn2_6/ptodata/1/ina/6A_COMB_seq:
4: /cgn2_6/ptodata/1/ina/6B_COMB_seq:
5: /cgn2_6/ptodata/1/ina/PCITS_COMB_seq:
6: /cgn2_6/ptodata/1/ina/backfile1_seq:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	70	4.2	7218	1	US-08-232-463-14		Sequence 14, Appl
c 2	48	2.9	2277	1	US-08-676-967-2		Sequence 2, Appl
c 3	48	2.9	2277	1	US-08-676-974-2		Sequence 2, Appl
c 4	48	2.9	2277	2	US-09-098-487-2		Sequence 2, Appl
c 5	42.2	2.5	2621	2	US-08-553-619B-8		Sequence 8, Appl
c 6	39.6	2.4	696	3	US-09-461-697-193		Sequence 193, Appl
c 7	39.6	2.4	699	3	US-09-161-697-191		Sequence 191, Appl
c 8	39.6	2.4	717	3	US-09-161-697-189		Sequence 189, Appl
c 9	39.6	2.4	774	3	US-09-161-697-187		Sequence 187, Appl
c 10	39.6	2.4	819	3	US-09-161-697-185		Sequence 185, Appl
c 11	39.6	2.4	1669	3	US-09-161-697-184		Sequence 184, Appl
c 12	39.2	2.4	719	3	US-08-714-918-11		Sequence 11, Appl
c 13	39.2	2.4	719	3	US-09-265-315-11		Sequence 11, Appl
c 14	39.2	2.4	719	3	US-09-266-412-11		Sequence 11, Appl
c 15	39.2	2.4	1850	3	US-08-617-866B-32		Sequence 32, Appl
c 16	39.2	2.4	2447	2	US-09-014-969-14		Sequence 14, Appl
c 17	39.2	2.4	4098	2	US-08-605-105-4		Sequence 4, Appl
c 18	39.2	2.4	1605	4	US-09-369-24-18		Sequence 18, Appl
c 19	38.6	2.3	273	4	US-09-134-001C-132		Sequence 132, Appl
c 20	38	2.3	2007	2	US-08-743-637B-169		Sequence 169, Appl
c 21	38	2.3	2007	3	US-09-526-80B-169		Sequence 1710, Appl
c 22	38	2.3	2028	4	US-09-134-001C-1710		Sequence 4, Appl
c 23	38	2.3	2422	1	US-07-367-106-5		Sequence 2, Appl
c 24	38	2.3	3138	1	US-07-867-106-4		Sequence 1, Appl
c 25	38	2.3	5852	1	US-09-557-884-2		Sequence 1, Appl
c 26	38	2.3	1830121	4	US-09-557-884-1		Sequence 1, Appl
c 27	37.8	2.2	1664976	4	US-08-916-421B-1		Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/082232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DONNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE: 26-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE: 26-AUG-1991
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 304/72/114 INRU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 1836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptz9pc-p1s
; US-08-232-463-14
Query Match 4.2%; Score 70; DB 1; Length 7218;

COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676,974
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman Ph.D., Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UCB96-055
 TELEPHONE: (415)343-4341
 TELEFAX: (415)343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2277 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-676-974-2

Query Match 2.9%; Score 48; DB 1; Length 2277;
 Best Local Similarity 26.1%; Pred. No. 0.0035; Mismatches 119; Indels 3; Gaps 1;
 Matches 205; Conservative 119; Mismatches 458; Indels 3; Gaps 1;

Db 811 GCNGTNAARMGNCCNGCNCNAARWSNWSNGAYCAYWSNGARGARGAYWSNGAY 870
 Qy 886 GCTGAAAGTACCAACTATAATGAAATTCCTTAAGGCGTACCGAGTACCGGT 945
 Db 871 GARGAWSNGAYWSNATHGAYGAGGNGARGAYTCNGCNCARWSNWSNARGAR 930
 Qy 946 GTAGATGATTCTAATGGAAACGGAAACCTTAATGAAACAAACAGTTCTGTAAG 1005
 Db 931 GARCARGARGAYAARGCNGTNCARGTWSNAYAARARMGNAARYTMCCNWSNGAY 990

Classification:
 RESULT 4
 US-09-098-487-2
 ; Sequence 2, Application US/09098487
 ; Patent No. 5917025
 ; GENERAL INFORMATION:
 ; APPLICANT: COLLINS, Kathleen
 ; TITLE OF INVENTION: Human Telomerase
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Science & Technology Law Group
 ; STREET: 268 Bush Street, Suite 1200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/098,487
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman Ph.D., Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UCB96-055
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)343-4341
 TELEX: (415)343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2277 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-098-487-2

Query Match 2.9%; Score 48; DB 2; Length 2277;
 Best Local Similarity 26.1%; Pred. No. 0.0035; Mismatches 119; Indels 3; Gaps 1;
 Matches 226; Conservative 119; Mismatches 458; Indels 3; Gaps 1;

Db 226 AACACACTGAAATGTTCTAACATATCCAGGAGTATGAAATTGCTAACAC 285
 Qy 214 AARATHAYTGNACNGTNGCVAARRAATGTTGNGAYAARACNARGANAR 273
 Db 286 TCGAAGGATAAAAGGAGCTCAAGAGATTCGCAAGCCAGAAAAGTCAGTAAAGC 345
 Qy 274 AAYGARAYWNGARTYTCNVAARARGCNAARGCNAARGTNGCNGAY 333
 Db 346 AAAGGACCATGCTGTTAACACATGACTCTAACATCTAACAGTCAAAGTCAA 405
 Qy 334 AARAARGCNCMENYNTNATHATHTNGNAAAYTWSNTTYAARTGYWSNGARGAYGAYTNAAR 393
 Db 406 AAAATCCCACTGATTTGAAAGCGGGTTAACAGATCTAACAGAACGGGGCAAT 465
 Qy 394 AONGNTTYGONCAPTYYGNGCNGTGYNTYBARGTNAAYATHCCNGNAAACCCNAYGNN 453
 Db 466 GATATATCTCCCTTCAGTGGGACCTTTCAGGACATTCCTGGTAAGGAGAA 525
 Qy 454 AARATGNGNNTT--YGGNTTYGNCARTTYAARAYTNTYNTBARGNGNAAARGCN 510
 Db 526 GCTACTGTTCTGACCTGAAGGCAAAAGATAATTCAACAGGGTTTGAGGCCAATGAA 585
 Qy 511 YTNAARGNNTAAATGAAARGARATAAARGNMGNACTGNGTNGAATGGCGNTIN 570
 Db 586 GCTGAGAGTACTCTTGACCAAAAAGCCAGGTATATGAGTCAGAGAGAA 645
 Qy 571 GONAARGAYAARTAYAARGAYAANCWSNGTWSNGCNAHGGGARGAARPNENCN 630
 Db 646 GAAATGTTGAAATACCTGAAACTGGGTATGAAACTGGCAAGATGCTGGCTGT 705
 Qy 631 GARWSNARCAVARGARWSNGTNAARAARARGGNGNGARGARGAYATGGARGAR 690
 Db 706 GATGTCAGCTTGTAGGGCAGCAACGATATCATGGTACTACCAATTAAAGGGCTC 765
 Qy 691 GARGARAYGAYGAGGAGAYGAGGAGYNTGNTYGAYGAYGAR 750
 Db 766 CCTGGAGAGTGGAAACAGTGGATGTCGGCAGCAAATGTCACCAAGGGAGGT 825
 Qy 751 GAYGARGARGARAYAARTAYAARGWSNAAARGTACCTGNGTARATCABRMGN 810
 Db 826 GAGTTTCATACCTCCCTGACCCCTCAAAAGGAAAGGAAAGGAGGGGACAAT 885
 Qy 806 AAAATCCCACTGATTGAGGGCAGGGTTATACGATCTCAAGAGAGGGGACAAT 465

394 ACNGTNTTYGCNCARTTYGGNGCNGTNYTNGARGTNAAAYATHCCNMGNAAARCCNGAYGGN 453
 Db ; TELEFAX: 415/857-1125
 Qy ; INFORMATION FOR SEQ ID NO: 8:
 Db ; SEQUENCE CHARACTERISTICS:
 Qy ; LENGTH: 2621 base pairs
 Db ; TYPE: nucleic acid
 Qy ; STRANDEDNESS: single
 Db ; TOPOLOGY: unknown
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

566 GATATATCTCCCTTCAGTGGGACGGCCAACCTTTAAGGACATTCTGGTAAAGGAA 525
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

454 AARATGMNGNTT--YGGNTTYGNCARTTYAARAYYTNYTNGARGCNGGNAAARGCN 510
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

526 GCTACTGGCTCTGACCTAGAAGGCAAAGATAATTCAACAGGCTTTCAGGCCAACTGTAA 585
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

511 YTNAAARGNATAAAYATGARARATAAARGNMGNAINGTNGINGTAAATGGGNGTN 570
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

586 GCTGAGAGTACTCATCTGACACAAAAAGCCAGGTTATAATGAGATTCAGAGAGAGAA 645
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

571 GCNAARGAYAARTAYARGAYACNCARWSNGTNWSNCNATHGGNGARARAARNSCAY 630
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

646 GAAATGTTGGAATAACATTGGAACACTTGGATGAAACTAGGCTCAAAGGGCAGATGCTGT 705
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

631 GARWSNAARACAYCARGARWSNGTNAAAARARARGNNGARGARGAYATGGGARGAR 690
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

706 GATGTCAGCCTGTAGGGCGAGCAAGATACTGGTGTGATGACATTAAAGGGCTC 765
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

691 GARGARAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGARGARGAYGAGYAYGAYGAR 750
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

766 CCTGGAAAGAAGGAAACAGAGTGGATGCTGGCAGCCAAATGCTCAGCAAGGGAGGT 825
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

751 GAYGARGARGARGARAYAATGARWSNAARGTNACNARCCNGTNCARATHCARAARMGN 810
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

826 GGTGTCATTAACCTCTGACGCCCTCAAAGAGAAAGGAAGGCGAGTAGTGTGTC 885
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

811 GCGTGNAAARMGNCCNGCNGCNGNAAFWNSNNGAYCAYWSNGARGARYG 870
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

886 GTGAAAGTACCAAACATAATAATAAATGCAAAATGGCAANGGCACTAACAGAAAGGT 945
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

871 GARGARNSNAYWSNATHGGAYGAYGNGNARGARYTNGCNCARWSNGAYC 930
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

946 GTAGATCATCTPAATAGGAAACCACTTAATGAAACAAAGCTTCTCTAGTAAG 1005
 Qy ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Db ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Qy ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Db ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Qy ; US-08-553-619B-8

931 GARCARGARGAYAARGCNGTNARGTNWSNAAAYAARARAAARNGNARYTNWSNGAY 990
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

1006 GGCAA 1010
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

991 GTNAA 995
 Db ; Query Match 2.5%; Score 42.2; DB 2; Length 2621;
 Qy ; Best Local Similarity 54.1%; Pred. No. 0.14;
 Db ; Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy ; ORGANISM: Chimeric tomato spotted wilt virus S RNA
 Db ; US-08-553-619B-8

RESULT 5
 US-08-553-619B-8
 Patent No. 5919705
 GENERAL INFORMATION:
 APPLICANT: DeHaan, Petrus T.
 TITLE OF INVENTION: Virus Resistant Plants
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5919/05artis Crop Protection
 STREET: 975 California Avenue
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.2.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,619B
 FILING DATE: December 1, 1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Marcus Myner, Lynn
 REGISTRATION NUMBER: 34,869
 REFERENCE/DOCKET NUMBER: 137-1082/FCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/354-3588

517 AAGGAGAGGACTACTGGTCTAACCTGAGCCAAATAATCAGGGTTGCGGG 576
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

528 AAAATGAAATGAGAAGGAGATGGAAATACTGGAAACTAGGTGAGATGGAAAGGGAGAA 596
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

568 AAGGGAAAGCTGGAAAGGAGAAGGAGAAGGAGAAGGAGAAGGAGAAGGAGAT 327
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

577 CCAAGTGAAGCTGAGAGTACTCATCTGACACAGGTTATAATGAGATCCCA 636
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

637 GAGAGAGAGAAATGGTGAATACTGGAAACTAGGTGAGATGGAAAGGGAGCA 696
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

638 GACGGAAAGGAAATGGAAAGGAGATGGAAAGGAGAAGGAGAAGGAGAAGGAGAA 447
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

697 GATGCTGTTGAGTCAGCTTGTAGGGCAGCAACCCGATATGGTAGTACCAATT 756
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

448 GACGAAAAGAAAACAGGAGTGGAAAGAGAATGAGATGAGAAGGAGATGAGA 507
 Db ; Query Match 2.4%; Score 39.6; DB 3; Length 696;
 Qy ; Best Local Similarity 43.6%; Pred. No. 0.37;
 Db ; Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Qy ; ORGANISM: Homo sapiens
 Db ; US-09-461-697-193

Qy 757 AAGGAGCTCCTGAAAGAACAGACTGGATGGTGGCAGCCAAAATGCTCACAA 816
 Db 508 AANGAGGAAAGATGTAAAGTCAAAGGAGATGAAAGAGAGAACATGAAAAGA 567
 Qy 817 GGGAGGTGAGTTCAATTACCTCTGGACCTCAAAGAGAAAGAGAGGAGT 876
 Db 568 GATCAAGGTGAAATGAGAAAGCTGGAAAAGAGAAAGTAAAGAGAGGA 627
 Qy 877 AGTGATGCGCTGAAACTATATGAAATTCTTAAATG 922
 Db 628 GAAGGAAGAGGAGATGAGATAAAGAGATGATGGAAAAG 673

RESULT 7

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
 ; DISORDERS, OR DISEASES INVOLVING

; FILE REFERENCE: 10001-005-999
 ; Patent No. 6277974
 ; GENERAL INFORMATION:
 ; APPLICANT: COGNENT NEUROSCIENCE, Inc.
 ; APPLICANT: Lo, Donald C.
 ; APPLICANT: Barney, Shawn
 ; APPLICANT: Thomas, Mary Beth
 ; APPLICANT: Portbury, Stuart D.
 ; APPLICANT: Katz, Lawrence C.
 ; NUMBER OF SEQ ID NOS: 466
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 189
 ; LENGTH: 717
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-461-697-191

Query Match 2.4%; Score 39.6; DB 3; Length 717;
 Best Local Similarity 43.6%; Pred. No. 0.37; Indels 0; Gaps 0;
 Matches 177; Conservative 0; Mi smatches 229;

Qy 517 AAAGGAGAGCTACTGGCTGACCTAGAGGAAAGATATTCAACAGGGTTGCAAGC 576
 Db 289 AAAGGGAAAGCTGAAAAGAGCAARGATGAAAGGGAAAGAGATGAAAGAGGAT 348
 Qy 577 CCAACTGAACTCTGAGAGTACTCTTGACACAAAAGCCAGGTATAATGAGATCCCA 636
 Db 349 AAAATGAAATGACAAAGGAGATGCAAAAGGAAGAAGATGAAAGAAAGTGA 408
 Qy 637 GAGAGAGAGAAAATGTTGAAATACCATTGAACTTGGATGAAACTGGATGAAACTGGCAAGAGGCA 696
 Db 409 GACGGAAAAGCAATGGAGAGATGAAAGAGAGAGATGAAAGAGAGGAA 468
 Qy 697 GATGGTGTGATGTGAGCCPTGTAGAGGGAGCAGATATCGTGTAGTACCAATT 756
 Db 469 GACACAAAAGAAAAGGGAGTGGAAAGAATGAGATGAAAGAGGGAGATAAA 528
 Qy 757 AAGGAGCTCCCTGGAGAGGAACAGTGGATGCTGCAGCCAAAATGCTCACAA 816
 Db 529 AAAGGGAAAGATGAAAGATGAAAGAGATGAAAGAGAGATGAAAGAGA 588
 Qy 817 GGGAGGTGAGTTCAATTACCTCTGACACAAAAGCCAGTTATATGATCCCA 636
 Db 331 AAAATGAAATGCAAAAGGAAAGATGCAAAAGGAAAGAATGCAAAAGGTGAA 390
 Qy 637 GAGAGAAAGAAATGGTAAATACCTTGGAAACTGGAAAGAGGCA 696
 Db 391 GACGAAAGGAATGGAGATGAAAGGAAAGTGAAGAAGTGAAGGAAAGAAGA 450
 Qy 697 GATGCTGTGATGTGACCTGTTGAGTGGCAACTATAATGAAATTCCTAAAAAT 922
 Db 649 GAAGGAAAAGGGAGATGATGATGTTGGAAAAAG 694

Query Match 2.4%; Score 39.6; DB 3; Length 699;

Best Local Similarity 43.6%; Pred. No. 0.37; Indels 0; Gaps 0;

Matches 177; Conservative 0; Mi smatches 229;

Qy 517 AAAGGAGAGCTACTGGCTGACCTAGAGGAAAGATATTCAACAGGGTTGCAAGC 576
 Db 271 AAAGGGAACTGGAAAAGAGCAAAAGTGAAAGGAGATGAAAGAGGAT 330
 Qy 577 CCAACTGAACTCTGAGAGTACTCATTTGACACAAAAGCCAGTTATATGATCCCA 636
 Db 331 AAAATGAAATGCAAAAGGAAAGATGCAAAAGGAAAGAATGCAAAAGGTGAA 390
 Qy 637 GAGAGAAAGAAATGGTAAATACCTTGGAAACTGGAAAGAGGCA 696
 Db 391 GACGAAAGGAATGGAGATGAAAGGAAAGTGAAGAAGTGAAGGAAAGAAGA 450
 Qy 697 GATGCTGTGATGTGACCTGTTGAGTGGCAACTATAATGAAATTCCTAAAAAT 922
 Db 451 GACGAAAGAAACAGGAGTTGGAAAAGAGATGAAAGAGAGGAGATAAA 510
 Qy 757 AAGGAGCTCCCTGGAGAGGAACAGTGGCTGCGAGTGGCAACAAATGCTCACAA 816
 Db 511 AAAGGGAAAAGATGAAAGGAGATGAAAGAGATGAAAGAGAGGAAAGAGA 570

Query Match 2.4%; Score 39.6; DB 3; Length 699;

Best Local Similarity 43.6%; Pred. No. 0.37; Indels 0; Gaps 0;

Matches 177; Conservative 0; Mi smatches 229;

Qy 817 GGGAGGTGAGTTCAATTACCTCTGACACAAAAGCCAGTTATATGATCCCA 876
 Db 571 GATGAGGTGAAAGGAGAAAGGAGATGAAAGGAGATGAAAGAGGAA 630
 Qy 877 AGTGATGCACTGTTGAGTGGCAACTATAATGAAATTCCTAAAAAT 922
 Db 631 GAAGGAAAAGGGAGATGATGAAAGAGATGATGGAAAAG 676

RESULT 8
 US-09-461-697-189
 ; Sequence 189, Application US/09461697
 ; Patent No. 6277974
 ; GENERAL INFORMATION:
 ; APPLICANT: COGNENT NEUROSCIENCE, Inc.
 ; APPLICANT: Lo, Donald C.
 ; APPLICANT: Barney, Shawn
 ; APPLICANT: Thomas, Mary Beth
 ; APPLICANT: Portbury, Stuart D.
 ; APPLICANT: Katz, Lawrence C.
 ; NUMBER OF SEQ ID NOS: 466
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 189
 ; LENGTH: 717
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-461-697-189

Query Match 2.4%; Score 39.6; DB 3; Length 717;
 Best Local Similarity 43.6%; Pred. No. 0.37; Indels 0; Gaps 0;
 Matches 177; Conservative 0; Mi smatches 229;

Qy 517 AAAGGAGAGCTACTGGCTGACCTAGAGGAAAGATATTCAACAGGGTTGCAAGC 576
 Db 289 AAAGGGAAAGCTGAAAAGAGCAARGATGAAAGGGAAAGAGATGAAAGAGGAT 348
 Qy 577 CCAACTGAACTCTGAGAGTACTCTTGACACAAAAGCCAGTTATAATGATCCCA 636
 Db 349 AAAATGAAATGCAAAAGGAAAGATGCAAAAGGAAAGAATGCAAAAGGTGAA 408
 Qy 637 GAGAGAGAGAAAATGTTGAAATACCATTGAAACTGGAAAGAGGCA 696
 Db 697 GATGCTGTGATGTGACCTGTTGAGTGGCAACTATAATGAAATTCCTAAAAAT 922
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
 ; DISORDERS, OR DISEASES INVOLVING

i TITLE OF INVENTION: CELL DEATH
 i FILE REFERENCE: 10001-005-999
 i CURRENT APPLICATION NUMBER: US/09/461,697
 i CURRENT FILING DATE: 1999-12-14
 i SEQ ID NUMBER: 450
 i SEQ ID NO: 466
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 187
 i LENGTH: 774
 i TYPE: DNA
 i ORGANISM: Homo sapiens
 i US-09-461-697-187

Query Match 2.4%; Score 39.6; DB 3; Length 774;
 Best Local Similarity 43.6%; Pred. No. 0.39;
 Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

Qy 517 AAAGGAGAAAGCTACTGGTCTGACCTAGAGCAAGATATTCAACAGGGTTTCAGGGC 576
 Db 391 AAAGGGAAAGCTGGAAAAGAGCAAGATGAAAGGGAAAGAATGGGAT 450

Qy 577 CCAGTGAAGCTGAGAGTACTCTGACACAAAAGCCAGTTATGATGATCCCA 636
 Db 451 AAAATGGAAATGAAAGAGATGCAAAAGGAAGAGATGGAAAAGGTGAA 510

Qy 637 GAGAGAGAAAGAAATGGTGGAAATACCATGGGAACTTGGGAAACTCGGAAAGAGGCA 696
 Db 511 GACGAAAGGAATGGAGAGATGAAAGAGAAAGGAAAGGAGAA 570

Qy 697 GATGCTGCTGATGAGCCCTTGTAGGGCAGCAAGPATCATGGTAGTACCAATT 756
 Db 571 GACGAAAGAAAGAGGTTGGAAAAGAGAAATGAGATGAAAGAGGAGATAAA 630

Qy 757 AAGGGACTCCCTGGAGAGAGGAAACAGGGTCAAGGTGAGGTTCTGCACCC 816
 Db 631 AAAGGGAAAGATGTAAGGATGAAAGATGAAAGGAGATGAAAGGAGAA 690

Qy 817 GGGAGGTGCAAGTTCACTACCCCTCTGCACCC 876
 Db 691 GATGAGGGAAAGTGGAAAGGAGAAAGCTGGAAGGAGAAAGATTTAAGAGAG 750

Qy 877 AGTGTGCGCTGAGTACCAACTATAATGAAATTCTCTAAATG 922
 Db 751 GAAGGAAAGGAGGAGATGAAAGATGAAAGGAGATGGAAAAG 796

RESULT 11
 US-09-461-697-184
 i Sequence 184; Application US/09461697
 i Patent No. 627794
 i GENERAL INFORMATION:
 i APPLICANT: COGENE NEUROSCIENCE, Inc.
 i APPLICANT: Jo, Donald C.
 i APPLICANT: Barney, Shawn
 i APPLICANT: Thomas, Mary Beth
 i APPLICANT: Portbury, Stuart D.
 i APPLICANT: Puranam, Kasturi
 i APPLICANT: Katz, Lawrence C.
 i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING,
 i TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
 i TITLE OF INVENTION: CELL DEATH
 i FILE REFERENCE: 10001-005-999
 i CURRENT APPLICATION NUMBER: US/09/461,697
 i CURRENT FILING DATE: 1999-12-14
 i NUMBER OF SEQ ID NOS: 466
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 184
 i LENGTH: 1669
 i TYPE: DNA
 i ORGANISM: Homo sapiens
 i US-09-461-697-184

RESULT 10
 US-09-461-697-185
 i Sequence 185; Application US/09461697
 i Patent No. 627794
 i GENERAL INFORMATION:
 i APPLICANT: COGENE NEUROSCIENCE, Inc.
 i APPLICANT: Jo, Donald C.
 i APPLICANT: Barney, Shawn
 i APPLICANT: Thomas, Mary Beth
 i APPLICANT: Portbury, Stuart D.
 i APPLICANT: Puranam, Kasturi
 i APPLICANT: Katz, Lawrence C.
 i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
 i TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
 i TITLE OF INVENTION: CELL DEATH
 i FILE REFERENCE: 10001-005-999
 i CURRENT APPLICATION NUMBER: US/09/461,697
 i CURRENT FILING DATE: 1999-12-14
 i NUMBER OF SEQ ID NOS: 466
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 185
 i LENGTH: 819

Query Match 2.4%; Score 39.6; DB 3; Length 1669;
 Best Local Similarity 43.6%; Pred. No. 0.55;
 Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

Qy 517 AAAGGAGAAAGCTACTGGTCTGACCTAGAGCAAGATATTCAACAGGGTTTCAGGGC 576
 Db 470 AAAGGGAAAGTGGAAAGAGATGAAAGGAAAGAATGGGAAAGAATGGAA 529

Qy 577 CCAAGTGAAGCTGAGAGTACTCTGACACAAAAGCCAGTTATGATGATCCCA 636
 Db 530 AAAATGGAAATGAAAGAGAAATGCAAAAGGAAAGAATGGAAAGAATGGAA 589

Qy 637 GAGAGAGAAAGAAATGGTGGAAATACCATGGGAACTTGGGAACTCGGAAAGAGGCA 696
 Db 590 GACGAAAGGAATGGAGAGATGCAAAAGGAGAAAGATGAAAGAGAAAGGAGAA 649

Query Match 2.4%; Score 39.6; DB 3; Length 819;
 Best Local Similarity 43.6%; Pred. No. 0.4;

Qy 697 GATGCTGTTGATGTCAGCTTGTAGGGCAGAACGATATCATGGTAGTACCAATT 756
 Db 650 GACGAAAAGAAACAGGAGGTGGAAAGAATGAAATGGAAAGAGAGGAGATAA 709
 Qy 757 AAGGAGCTCCCTCGAAGGAAACAGAGTCGATGCTGGCCAAATAGCTCACCA 816
 Db 710 AAAGAGGGAAAGATGTAAGATGAAAGATGAAAGAGATGAAAGAGATGAAAGA 769
 Qy 817 CGGAAGGTTGAGTTTCATTACCTCCMGCACCTCAAAGAGAAAAGAGGAGT 876
 Db 770 GATGAACTGGAATAGGAAAGAGCTGGAAAGAGAGACATTAAGAGAGGAA 829
 Qy 877 AGTGATGGAGCTGAAAGTACCAACTATAATGAAATTCTAAATG 922
 Db 830 GAGGGAAAAGGGAGAGATGAGTCAAGAGATGATGAAAGAG 875

RESULT 13

US-09-714-918-11/c

Sequence 11, Application US/08714918

Patent No. 6037123

GENERAL INFORMATION:

SEQUENCE: Sequence 11, Application US/08714918

PRIORITY: US-09-714-918-11/c

FILING DATE: September 13, 1996

CLASSIFICATION: 424

PRIORITY NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE DOCKET NUMBER: 222/005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-714-918-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

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REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/24

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TELEFAX: (213) 955-0440

TELELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

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FILING DATE: September 15, 1995

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NAME: Warburg, Richard J.

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REFERENCE/DOCKET NUMBER: 224/24

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TELEFAX: (213) 955-0440

TELELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

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FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

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NAME: Warburg, Richard J.

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REFERENCE/DOCKET NUMBER: 224/24

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TELEFAX: (213) 955-0440

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INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/24

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TELEFAX: (213) 955-0440

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SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

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FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

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NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/24

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TELEFAX: (213) 955-0440

TELELEX: 67-3510

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SEQUENCE CHARACTERISTICS:

LENGTH: 719 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/24

TELECOMMUNICATION INFORMATION:

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TELEFAX: (213) 955-0440

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TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-11

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

Qy 1489 AATGTTTAAGCAAAAAATCATTACAGATCTATGAAATAGCTAACATTGAGTAGC 1548
Db 378 ACTAAGTTCTATTCAACATTAACTTATGAACTATGAAATAGCTAACATTGAGTAGC 319
Qy 1549 TGTCAATTAAAAATAGTTGCTGAATGTCAACAAATGCCCTCTATGTTGCTCTGTAGA 1608
Db 318 GAGTATAAAAAGCACTTGTGCAAAAACACAAAGTGCCTAAACTTAATTATTTCACT 259
Qy 1609 CATGAAATAAA 1620
Db 258 AGTTTGATCAA 247

Search completed: November 29, 2003, 18:15:24
Job time : 110 secs

Result No.	Score	Query	Match	Length	DB	ID	Description	§
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2	163.8	99.0	1969	12	US-09-794-422-33	Sequence 45, Appli	Sequence 45, Appli	
3	163.8	99.0	2019	12	US-09-794-422-45	Sequence 5, Appli	Sequence 5, Appli	
4	163.8	99.0	2112	12	US-09-794-422-7	Sequence 7, Appli	Sequence 7, Appli	
5	136.9	82.7	1662	12	US-10-311-840-3	Sequence 3, Appli	Sequence 3, Appli	
6	128.9	77.9	1575	12	US-10-311-840-2	Sequence 2, Appli	Sequence 2, Appli	
7	514.8	31.1	1655	12	US-09-794-422-1	Sequence 1, Appli	Sequence 1, Appli	
8	485.2	29.3	1682	12	US-09-794-422-3	Sequence 3, Appli	Sequence 3, Appli	
9	60	3.6	60	12	US-09-905-975-16013	Sequence 16013, A	Sequence 16013, A	
c 10	47.6	2.9	3677378	12	US-10-312-841-1	Sequence 1, Appli	Sequence 1, Appli	
c 11	46.8	2.8	345	12	US-09-814-353-15466	Sequence 5466, AP	Sequence 5466, AP	
c 12	46.8	2.8	345	12	US-09-814-353-11793	Sequence 11793, A	Sequence 11793, A	
c 13	46.6	2.8	2826	12	US-10-032-585-6930	Sequence 6930, AP	Sequence 6930, AP	
c 14	45.8	2.8	2000	10	US-09-887-576-831	Sequence 831, AP	Sequence 831, AP	
c 15	44.8	2.7	3673778	12	US-10-312-841-2	Sequence 2, Appli	Sequence 2, Appli	
c 16	44.6	2.7	349	12	US-09-814-353-18039	Sequence 18039, A	Sequence 18039, A	

Db	GGCCAGTCAGTGAATGCGATTAAACTCCCTGGGAGAAAACAAGAGAACACACCTAGAAATG	571	Qy	13.22 GTCCTGGAGACCCCTGTCACCTCTGAGTTGATGTAGAGGAGGCCCTGACAGCTGACCCAG	1.381
Qy	242 TTCTAAACATTAATCCTCAGCAAGTATGCTAAAGCTAACACTCGAAGGATAAAAAGA	301	Db	1652 GTCCTGGAGACCCCTGTCACCTCTGAGTTGATGTAGAGGAGGCCCTGACAGCTGACCG	1.711
Db	572 TTCTAAACATTAATCCTCAGCAAGTATGCTAAAGCTAACACTCGAAGGATAAAAAGA	631	Qy	13.82 GTGAAGGAGGAGATAGAGTGGAAACTGAGTGGCCAGAAATCCTGGCTCTCTGGGAA	1.441
Qy	302 AGCCCTAAAGAGATTCCAGCCAGAAAGTCCAGTAAMAGCAAAAGCAGCCATCGTA	361	Db	1712 GTGAAGGAGGAGATAGAGTGGAAACTGAGTGGCCAGAAATCCTGGCTCTCTGGGAA	1.771
Db	632 AGCCCTAAAGAGATTCCAGCCAGAAAGTCCAGTAAMAGCAAAAGCAGCCATCGTA	691	Qy	1442 TTTCCTGCTATCTTAAACTACAGTAAAGCTTAAATCTCTAAAGCTTAAATGTTTAAGC	1.501
Qy	362 TTCAAGCAAAACATGGACTACCTAAACATCTCTCAAAAGTCAAAATCCAGTGTAT	421	Db	1772 TTTCCTGCTATCTTAAACTACAGTAAAGCTTAAATCTCTAAAGCTTAAATGTTTAAGC	1.831
Db	692 TTCAAGCAAAACATGGACTACCTAAACATCTCTCAAAAGTCAAAATCCAGTGTAT	751	Qy	1502 AAAAAGAAATCATTACAGATCTATGAAATAGCTAACTTGGAGTGTGATTAAAGAA	1.561
Qy	422 TTGAAGGCGCCGTTATACTAGATCTCAAGAGAGGAACTGATGATATACTCCCTTC	481	Db	1832 AAAAAGAAATCATTACAGATCTATGAAATAGCTAACTTGGAGTGTGATTAAAGAA	1.891
Db	752 TTGAAGGCGCCGTTATACTAGATCTCAAGAGAGGAACTGATGATATACTCCCTTC	811	Qy	1562 TAGTTGGTGAATGTCACAAATGCCCTCTATGTTGTTGCTCTGAGCATGAAATAAAC	1.621
Qy	482 GTGGGGACGGCCAACCTTTAGGACATTCCTCTGTAAGGAGAAGGCTACTGGTCTGTGAC	541	Db	1892 TAGTTGGTGAATGTCACAAATGCCCTCTATGTTGTTGCTCTGAGCATGAAATAAAC	1.951
Db	812 GTGGGGACGGCCAACCTTTAGGACATTCCTCTGTAAGGAGAAGGCTACTGGTCTGTGAC	871	Qy	1622 AATATCTCTGATGATAA	1.639
Qy	542 TAGAGGCAALAGATATTCAAACAGGGTTGAGGCCAACATGAGCTGAGGTACTCATC	601	Db	1922 AATATCTCTGATGATAA	1.969
Db	872 TAGAGGCAALAGATATTCAAACAGGGTTGAGGCCAACATGAGCTGAGGTACTCATC	931			
Qy	602 TTGACACAAAAAGCCAGGTTATACTAGATCCAGAGGAAAGAAATGGTGGAAATA	661		RESULT 3	
Db	932 TTGACACAAAAAGCCAGGTTATACTAGATCCAGAGGAAAGAAATGGTGGAAATA	991		US - 09 - 794 - 422 - 5	
Qy	662 CCATTGGAAACTTGGGATGAAACTGGCAAAGGGCAATGGCTGTTGATGTCAGCCCTGTAG	721		; Sequence 5, Application US/09794422	
Db	992 CCATTGGAAACTTGGGATGAAACTGGCAAAGGGCAATGGCTGTTGATGTCAGCCCTGTAG	1051		; Publication No. US20030166239A1	
Qy	722 AGGGACCAACCATATCTGGTACCAATTAGGACTCCCTGGAGGAGGAA	781		; CURRENT APPLICATION NUMBER: US/09/794,422	
Db	1052 AGGGACCAACCATATCTGGTACCAATTAGGACTCCCTGGAGGAGGAA	1111		; PRIORITY FILING DATE: 2001-02-27	
Qy	782 ACAGAGTGGATCTGGCAACCAAATCTCAACAGGAAGTTGACTTCATTACCTC	841		; PRIORITY APPLICATION NUMBER: 60/185,617	
Db	1112 ACAGAGTGGATCTGGCAACCAAATCTCAACAGGAAGTTGACTTCATTACCTC	1171		; PRIORITY FILING DATE: 2000-02-29	
Qy	842 CTGCACCCCTAAAGAGAAAAGGAGGAGGCTGAGCTGAAAGTACCAACT	901		; PRIORITY APPLICATION NUMBER: 60/234,500	
Db	1172 CTGCACCCCTAAAGAGAAAAGGAGGAGTACTGTCAGCTGAAGTACCAACT	1231		; PRIORITY FILING DATE: 2000-09-22	
				; NUMBER OF SEQ ID NOS: 46	
				; SEQ ID NO: 5	
				; LENGTH: 2019	
				; TYPE: DNA	
				; ORGANISM: Homo sapiens	
				US - 09 - 794 - 422 - 5	
			Query Match	99.0%	Score 1638; DB 12; Length 2019;
			Best Local Similarity	100.0%	Pred. No. 0; Indels 0; Gaps 0;
			Matches 1638;	Conservative 0; Mismatches 0;	
Qy	2 TCAATTAAGAAATAGTATGTTGATCTACATGAAAGCAATACTCACATGGCTGAGGATGTCAA	61			
Db	382 TGAATTAAGAAATAGTATGTTGATCTACATGAAAGCAATACTCACATGGCTGAGGATGTCAA	441			
Qy	62 TTATCTTAAGTCAACTGGATAAGGTTGAGGATGGATGTTGAGCTACATGAAATACTGCAAA	121			
Db	442 TTATCTTAAGTCAACTGGATAAGGTTGAGGATGGATGTTGAGCTACATGAAAC	501			
Qy	122 TACATGACCAAGAAAGATAATGCGCAGCTCTCATGAAATAACATATAATATGG	181			
Db	502 TACATGACCAAGAAAGATAATGCGCAGCTCTCATGAAATAACATATAATATGG	561			
Qy	182 GCGCAGTGACTGGCATTAACCTGGGAGAAAGAACAGAGACACCTAGGATG	241			
Db	562 GCGCAGTGACTGGCATTAACCTGGGAGAAAGAACAGAGACACCTAGGATG	621			
Qy	242 TTCTAAACATAATCCAGCAAGTATGCTAAAGGCAACTCGAAGGATAAAAAGA	301			
Db	1592 TTCTAAACATAATCCAGCAAGTATGCTAAAGGCAACTCGAAGGATAAAAAGA	1651			

Db	622	TCTAAACATAATCCCAGCAAGTATGAACTCTAAAGCACACTCGAAGGGATAAAAAGA	681	Qy	1382	GTCAGAGAGGATAGAGTGAAGAAACTGAGTGAGCCAAAAGAATCCTGGTCTCCCTGGGGAA	1441		
Qy	302	AGCCTCAAAAGAGATTCCCAAGGCCAGAAAGTCCAGTAAAGCRAAAGCACCCATGTA	361	Db	1762	GTCAGAGAGGATAGAGTGAAGAACTGAGTGAGCCAAAAGAATCCTGGTCTCCCTGGGGAA	1821		
Db	682	AGCCTCAAAAGAGATTCCCAAGGCCAGAAAGTCCAGTAAAGCRAAAGCACCCATGTA	741	Qy	1442	TTTTTGTATCTTAATGTCAGTAAAGCTATAAACTTAAAGCTATAATGTTTGTAGC	1501		
Qy	362	TTCACACAAACATTTGATCACTTCAAAAGTCAAAAAAATCCCAGTGTATT	421	Db	1822	TTTTTGTATCTTAATGTCAGTAAAGCTATAAACTTAAAGCTATAATGTTTGTAGC	1881		
Db	742	TTCACACAAACATTTGATCACTTCAAAAGTCAAAAAAATCCCAGTGTATT	801	Qy	1502	AAAAAAATCATTACGATCATGALATAGTAAACATTGAGTAACTTAA	1561		
Qy	422	TTCAGGGAGCGTTTATCAGATCTTCAGAGAGGGACATGATATCTCCCTTCA	481	Db	1882	AAAAAAATCATTACGATCATGALATAGTAACTTAA	1941		
Db	802	TTGAGGGAGGGTTTATCAGATCTTCAGAGGGACATGATATCTCCCTTCA	861	Qy	1562	TAGTTGGTGAATTCACAAATGCTATGTTGCTGTAGACATGAAATTAAC	1621		
Qy	482	GTGGGGACGCCAACCTTTAAGCACATTCTGTAAAGGAGAGCTACTGGCTCTGAC	541	Db	1942	TAGTGGTGAATTCACAAATGCTATGTTGCTGTAGACATGAAATTAAC	2001		
Db	862	GTGGGGACGCCAACCTTTAAGCACATTCTGTAAAGGAGAGCTACTGGCTCTGAC	921	Qy	1622	AATATCTCTGATGATAA	1639		
Qy	542	TAGAGGCCAAAGATAATTCAAAACGGTTGCAGCCCAAGTGAAGCTACTCATC	601	Db	2002	AATATCTCTGATGATAA	2019		
Db	922	TAGAGGCCAAAGATAATTCAAAACGGTTGCAGCCCAAGTGAAGCTACTCATC	981	RESULT 4					
Qy	602	TTCAGACAAAAAAGCCAGTTTATGAGATCCAGAGAGAAATACTGGTGGAAATA	661	US-09-794-422-7					
Db	982	TTGACACAAAAAAGCCAGTTTATGAGATCCAGAGAGAAATACTGGTGGAAATA	1041	; Sequence 7, Application US/09794422					
Qy	662	CCATTGGGAACTTGGGATTAACCTGGCAAGAGCCAGACCTGCTGTGATCTGAGCTTGTAG	721	; Publication No. US20030166239A1					
Db	1042	CCATTGGGAACTTGGGATTAACCTGGCAAGAGCCAGACCTGCTGTGATCTGAGCTTGTAG	1101	; GENERAL INFORMATION:					
Qy	722	AGGGCAGGCCAGATACTGGGATGATCTGGGATGATCTGGGATGATCTGGGATG	781	; APPLICANT: Brown, Thomas A.					
Db	1102	AGGGCAGGCCAGATACTGGGATGATCTGGGATGATCTGGGATGATCTGGGATG	1161	; DE WET, Jeffrey R.					
Qy	782	ACAGAGTGGATGCTGGCACCCAAATGCTACCAAGGGAGTTGAGTTCTACCCCT	841	; APPLICANT: Gowen, Lori C.					
Db	1162	ACAGAGTGGATGCTGGCACCCAAATGCTACCAAGGGAGTTGAGTTCTACCCCT	1221	; APPLICANT: Hames, Lynn M.					
Qy	842	CTGGAACCCCTCAAAAGAACAAAGAACAAAGAACGGCACTGATGCGCTGAAGTACACT	901	; TITLE OF INVENTION: Maumillian Osteoregulins					
Db	1222	CTGGAACCCCTCAAAAGAACAAAGAACAAAGAACGGCACTGATGCGCTGAAGTACACT	1281	; FILE REFERENCE: PC10445					
Qy	902	ATAATGAAATTCTTAAATGGCAAAAGGAGGCACTGATGCGCTGAAGTACACT	961	; CURRENT APPLICATION NUMBER: US/09794422					
Db	1282	ATAATGAAATTCTTAAATGGCAAAAGGAGGCACTGATGCGCTGAAGTACACT	1341	; CURRENT FILING DATE: 2001-02-27					
Qy	962	GGACCAAGCAACCTTAAATGAAACAAAGTTCCCTGATACGGCAAAAGTCAGGCC	1021	; PRIORITY APPLICATION NUMBER: 60/185,617					
Db	1342	GGACCAAGCAACCTTAAATGAAACAAAGTTCCCTGATACGGCAAAAGTCAGGCC	1401	; PRIORITY FILING DATE: 2000-02-29					
Qy	1022	TGCCCATTCCTCTCGTGGCTCTGATGATCTGTTGATGAACTTGGCTTAAATG	1081	; PRIORITY APPLICATION NUMBER: 60/234,500					
Db	1402	TGCCCATTCCTCTCGTGGCTCTGATGATCTGTTGATGAACTTGGCTTAAATG	1461	; PRIORITY FILING DATE: 2000-09-22					
Qy	1082	GCCCCAGTGTATGAGATAATAACATGGCAGAAATAATGATGTTACCCACAGAC	1141	; NUMBER OF SEQ ID NOS: 46					
Db	1462	GCCCCAGTGTATGAGATAATAACATGGCAGAAATAATGATGTTACCCACAGAC	1521	; SEQ ID NO 7					
Qy	1142	AAAATAATTCTACAGGATAAGGTTATGCAACAGGAAAGGTCTCTGTTAAATG	1201	; LENGTH: 2112;					
Db	1522	AAAATAATTCTACAGGATAAGGTTATGCAACAGGAAAGGTCTCTGTTAAATG	1581	; Best Local Similarity: 100.0%; Pred. No. 0;					
Qy	1202	CCCATTCACAGGAGTTACAGGATAAGGTTATGCAACAGGAAAGGTCTCTGTTAAATG	1261	; Mi matches: 0; Indels: 0; Gaps: 0;					
Db	1582	CCCATTCACAGGAGTTACAGGATAAGGTTATGCAACAGGAAAGGTCTCTGTTAAATG	1641	; 2 TGAATTAACAAAGAGATAAGGTTATGCAACAACTATGCTGAGGATGCTATGCAAAC					
Qy	1262	GTGGCAGTGTAAAGTGGCGATGTTGACTTCCACCGAGGAATGCTCCAGGGGTGAC	1321	; 475 TGAATTAACAAAGAGATAACTCAACATGCTGAGGATGCTAACTGCAAAC					
Db	1642	GTGGCAGTGTAAAGTGGCGATGTTGACTTCCACCGAGGAATGCTCCAGGGGTGAC	1701	; 62 TTATTCCTTAATGCTGAGTGTGATGCTGAGGATGCTATGCTGAGGATGCTAACTGCAAAC					
Qy	1322	GTCTGAAGGACTCTGTCACCTGACTGTTGACTTGAAGGAGGCCACTGAGCTGAC	1381	; 595 TACATGACCAAGAGATAATGCTGAGGATGCTATGCTGAGGATGCTAACTGCAAAC					
Db	1702	GTCTGAAGGACTCTGTCACCTGACTGTTGAGTGTGAGCTGAGGAGGCCACTGAGC	1761	; 535 TTATCCCTAGTCACCTGGGATTAAGGTTGAGGATGCTATGCTGAGGATGCTAACTGCAAAC					
Qy	302	AGCCCTAAAGAGATTCCCAAGGCCAAGAAAGTCCGTTGAGTGTGAGCTGAC	361	; 182 GGCCAGTGTACTGCTTAAACTCCTGGGAGAAACAGAGACACCTAGGANT					
Db				; 655 GGCCAGTGTACTGCTTAAACTCCTGGGAGAAACAGAGACACCTAGGAAATG					
Qy				; 242 TTCTAAACATAATCCAGGAAGTGTGATTTATGCTGAGGATGCTAACTGCAAAC					
Db				; 715 TTCTAAACATAATCCAGGAAGTGTGATTTATGCTGAGGATGCTAACTGCAAAC					
Qy				; 774 AGCTGAAAGGACTCTGTCACCTGACTGTTGAGTGTGAGCTGAGGAGGCCACTGCTTA					

Db	775	AGCCCTAAAGAGGATTCCOAGGCCAGAAAGTCAGTAAAGCAAAAGCACCCATGTTA	834	Qy	1442	TTTTGGCTATCTTAATAGTCACAGTATAAAATTCTATTAAAGCTATAATGTTTTAGC	1501
Qy	362	TTCACACAAATTGACTTAAACATCTCTCAAAGTCAAAAAAATCCCACTGATT	421	Db	1515	TTTTGGCTATCTTAATAGTCACAGTATAAAATTCTATTAAAGCTATAATGTTTTAGC	1974
Db	835	TTCACACAAATTGACTTAAACATCTCTCAAAGTCAAAAAAATCCCACTGATT	894	Qy	1502	AAAAAAAATCTTAAAGATCTTAAAGATGAAATAGTTGAGTAACTTGTGTCATTAA	1561
Qy	422	TGAGGGCGCGTTATACTGACTCTCAAGAGAGGGCAATGATATACTCTTTCA	481	Db	1975	AAAAAAAATCTTAAAGATCTTAAAGATGAAATAGTTGAGTAACTTGTGTCATTAA	2034
Db	895	TGAGGGCGCGTTATACTGACTCTCAAGAGAGGGCAATGATATACTCTTTCA	954	Qy	1562	TAGTTGGTGAATGTCAGAAATGCTCTAGTTGTTGCTCTAGTGTGACATGAAATAC	1621
Qy	482	GTGGGAGCGCCAACTTAAAGGACATTCTGGTAAAGGAGGAAGCTACTGTCCTGAC	541	Db	2035	TAGTTGGTGAATGTCAGAAATGCTCTAGTTGTTGCTCTAGTGTGACATGAAATAC	2094
Db	955	GTGGGAGCGCCAACTTAAAGGACATTCTGGTAAAGGAGGAAGCTACTGTCCTGAC	1014	Qy	1622	AAATATCTCGATGATAA	1639
Qy	542	TAGAAGGCAAAAGATAATTCAACAGGGTTGGAGGCCAAAGTCAGTGAAGTACTCATC	601	Db	2095	AAATATCTCGATGATAA	2112
Db	1015	TAGAAGGCAAAAGATAATTCAACAGGGTTGGAGGCCAAAGTCAGTGAAGTACTCATC	1074				
Qy	602	TGACACAAAGCCAGGTTATAATGAGATCCAGAGAGAGAAATGTTGGAATA	661		RESULT 5		
Db	1075	TGACACAAAGCCAGGTTATAATGAGATCCAGAGAGAAATGTTGGAATA	1134		US-10-311-840-3		
Qy	662	CCATTGGAACTAGGGATGAAACTCTGGAAAGGGCAGATGTTGATGTCAGCCTGTAG	721		/ Sequence 3, Application US/10311840		
Db	1135	CCATTGGAACTAGGGATGAAACTCTGGAAAGGGCAGATGTCAGCCTGTAG	1194		/ PUBLICATION NO. US20030175808AI		
Qy	722	ACGGCAGCAACGATATCATGGTGTACCAATTAAAGGAGCTCCCTGGAAAGAGGAA	781		/ GENERAL INFORMATION:		
Db	1195	ACGGCAGCAACGATATCATGGTGTACCAATTAAAGGAGCTCCCTGGAAAGAGGAA	1254		/ APPLICANT: KUROKAWA, Tomofumi		
Qy	782	ACAGAGTCGATGTCGCAAGCCAAAATGCTACAAAGGAAGGTGAGTTGATCCTC	841		/ APPLICANT: YAMADA, Takao		
Db	1255	ACAGAGTCGATGTCGCAAGCCAAAATGCTACAAAGGAAGGTGAGTTGATCCTC	1314		/ APPLICANT: MORIMOTO, Shigeto		
Qy	842	CTGCACCCCTAAAGAGAAAGAAAGGAGGAGTGTAGTCAGTGAAGTACCAACT	901		/ TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA		
Db	1315	CTGCACCCCTAAAGAGAAAGAAAGGAGTGTAGTCAGTGAAGTACCAACT	1374		/ FILE REFERENCE: 2738US0P		
Qy	902	ATAATGAAATTCTAAATGGAAAAGCCTAACCCATGTTAATA	961		/ CURRENT APPLICATION NUMBER: US/10/311-840		
Db	1375	ATAATGAAATTCTAAATGGAAAAGCCTAACCCATGTTAATA	1434		/ CURRENT FILING DATE: 2002-12-18		
Qy	962	CGAACCAAGCACCTTAAATGAAAAAAAGTTCTTAAAGGCAAAAGTCAGGCC	1021		/ PRIOR APPLICATION NUMBER: PCT/JP01/05263		
Db	1435	CGAACCAAGCACCTTAAATGAAAAGCCTAACCCATGTTAATA	1494		/ PRIOR FILING DATE: 2001-06-20		
Qy	1022	TGCCATTCTCTCTGTTGCTGTGATATGAAATCAAACCAATTGTTCTTTAATG	1081		/ PRIOR APPLICATION NUMBER: JP 2000-191088		
Db	1495	TGCCATTCTCTCTGTTGCTGTGATATGAAATCAAACCAATTGTTCTTTAATG	1554		/ NUMBER OF SEQ ID NOS: 10		
Qy	1082	GCCCCAGCTATGAAATAATAAAACATGGCAAAATATCATGGCAACGAC	1141		/ SEQ ID NO 3		
Db	1555	GCCCCAGCTATGAAATAATAAAACATGGCAAAATATCATGGCAACGAC	1614		/ LENGTH: 1662		
Qy	1142	AAATAATTCTACCGATAAGGTTGCCAAAGGAAAGGCTCTGGGTAGAAC	1201		/ TYPE: DNA		
Db	1615	AAATAATTCTACCGATAAGGTTGCCAAAGGAAAGCTCTGGGTAGAAC	1674		/ ORGANISM: Human		
Qy	1202	CCATTCCAAACAGGATTCTGTTGCTGTGATATGAAATCAAACCAATTGTTCTTTAATG	1261		/ US-10-311-840-3		
Db	1675	CCATTCCAAACAGGATTCTGTTGCTGTGATATGAAATCAAACCAATTGTTCTTTAATG	1734				
Qy	1262	GPGGCAGTTCACTGAGGGATGGTAACTAGTCCAGGGTTCCAGGGTGA	1321				
Db	1735	GPGGCAGTTCACTGAGGGATGGTAACTAGTCCAGGGTTCCAGGGTGA	1794				
Qy	1322	GTCTGAAGACCTCTGTCACCTGTCAGTTGAGGAGGCCACCTGACAGCTGAC	1381				
Db	1795	GTCTGAAGACCTCTGTCACCTGTCAGTTGAGGAGGCCACCTGACAGCTGAC	1854				
Qy	1382	GTGAAGGAGGATGAGTAAAGGAAAGCTAGTGTAGGAGGCCAGAAATCTGTC	1441				
Db	1855	GTGAAGGAGGATGAGTAAAGGAAAGCTAGTGTAGGAGGCCAGAAATCTGTC	1914				

Qy	422	TTGAGGAGGGTTATAAGGATCTTCAAGAGGGGAAATATACTCTTTCA	481
Db	714	TTGAGGAGGGTTATAAGGATCTTCAAGAGGGGAAATATACTCTTTCA	773
Qy	482	GTGGGAGCGCCAACTTTAAGGACATTCTGTTAAAGGAGAACCTA	541
Db	774	GTGGGAGCGCCAACTTTAAGGACATTCTGTTAAAGGAGAACCTA	833
Qy	542	TAGAGGCAAGATATTCAAACAGGTTTGCAGGCCAACTGAACTGAGAGTACTCATC	601
Db	834	TAGAGGCAAGATATTCAAACAGGTTTGCAGGCCAACTGAACTGAGAGTACTCATC	893
Qy	602	TTCACACAAAACCAGGTTTATGATGAGTCCPAGAGAAAGAAATGGAAATA	661
Db	894	TTCACACAAAACCAGGTTTATGATGAGTCCPAGAGAAAGAAATGGAAATA	953
Qy	662	CCATTGGAACTTGGATGAAACTGGCAAAGGGCAGATGGTGTGATGTCA	721
Db	954	CCATTGGAACTTGGATGAAACTGGCAAAGGGCAGATGGTGTGATGTCA	1013
Qy	722	AGGCAGCAACGATATCATGGTGTGATCCTGGTAAAGAGAGGAA	781
Db	1014	AGGCAGCAACGATATCATGGTGTGATCCTGGTAAAGAGAGGAA	1073
Qy	782	ACAGGTGATGTCGGAGCCAAATTGCTACCAAGGAGTTGATGTCATACCTCT	841
Db	1074	ACAGGTGATGTCGGAGCCAAATTGCTACCAAGGAGTTGATGTCATACCTCT	1133
Qy	842	CTGCACCCCTCAAAAGGAAAGGAAAGGAAAGGCAATAGTGTGAC	901
Db	1134	CTGCACCCCTCAAAAGGAAAGGAAAGGCAATAGTGTGAC	1199
Qy	902	ATATGAAATTCCCTAAATTGGCAAAAGGCCATACAGAAAGGCTGTAGATCTTAATA	961
Db	1194	ATATGAAATTCCCTAAATTGGCAAAAGCCATACAGAAAGGCTGTAGATCTTAATA	1253
Qy	962	GGAAACCAAGAACCTTAATGAAACAAAGGTCTCTAGTAAGGCCAAGGTCTGGCC	1021
Db	1254	GGAAACCAAGAACCTTAATGAAACAAAGGTCTCTAGTAAGGCCAAGGTCTGGCC	1313
Qy	1022	TGCCATTCTCTCTGTTGATATAATGAAATCAAAGGAAATGGATTCCCTTAATG	1081
Db	1314	TGCCATTCTCTCTGTTGATATAATGAAATCAAAGGAAATGGATTCCCTTAATG	1374
Qy	1082	GCCCGAATGATGAGBATAATAACACATGGCAAGAAATATCATPATGTA	1141
Db	1374	GCCCGAATGATGAGBATAATAACACATGGCAAGAAATATCATPATGTA	1433
Qy	1142	AAATAATTCTACAGGAAATAGGTATGCAACAGGAAGGCTCTGGGTAAACAA	1201
Db	1434	AAATAATTCTACAGGAAATAGGTATGCAACAGGAAGGCTCTGGGTAAACAA	1493
Qy	1202	CCCATTCACAGGGTTAGTCCCTGTTAGGATGAGTCATCTGACA	1261
Db	1494	CCCATTCACAGGGTTAGTCCCTGTTAGGATGAGTCATCTGACA	1555
Qy	1262	GTGGCACTTCAGTAGGGCATGGTCACTAGTCCACAGGAGTCCAGGGGTGACA	1321
Db	1554	GTGGCACTTCAGTAGGGCATGGTCACTAGTCCACAGGAGTCCAGGGGTGACA	1613
Qy	1322	GTCTGAAGAACCTCTGTCACCTGTGACATTGTAAGGAGGCCACCTG	1370
Db	1614	GTCTGAAGAACCTCTGTCACCTGTGACATTGTAAGGAGGCCACCTG	1662

RESULT 6
US-10-311-840-2
; Sequence 2, Application US10311840
; Publication No. US2003017508A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takaو
; APPLICANT: MURAMOTO, Shigeto

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; TITLE OF INVENTION: No. US20130175808A1 Protein and its DNA
; FILE REFERENCE: 2738US0P
; CURRENT APPLICATION NUMBER: US10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-2

Query Match 77.9%; Score 1289; DB 12; Length 1575
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1289; Conservative 0; Mismatches 0; Indels 0

Qy 2 TGATAAAGAATAATGATCTACTAACAGAATACTCACAACTGCCTGAA
Db 287 TGATAAAGAATAATGATCTACTAACAGAATACTCACAACTGCCTGAA
Qy 62 TTTATCCTAAGCTCAACTCGGATAAAGGTTTGAGATTCGAGATGATGCTA
Db 347 TTATATCCTAAGTCAAATCTGGATAAAGGTTTGAGATGGAGATGATGCTA
Qy 122 TATATGACCAAGAAGAATACTGGCAAGCTCATCGAAATAACATGCAAC
Db 407 TATATGACCAAGAAGAATACTGGCAAGCTCATCGAAATAACATGCAAC
Qy 182 GGCCAGTGTACTCGGATTAACCTCTGGGGAAACAAAGAGAACACAC
Db 467 GGCCAGTGTACTCGGATTAACCTCTGGGGAAACAAAGAGAACACAC
Qy 242 TTCTAAACATAATCCCGCAACTGTAATGTTTAAAGCTTAAAGGAACTCGAGG
Db 527 TTCTAAACATAATCCCGCAACTGTAATGTTTAAAGCTTAAAGGAACTCGAGG
Qy 302 AGCCTAAAGAATTCGGAGCCAGAAATGTCAGTAAAGCAAAAGGCA
Db 587 AGCCTAAAGAATTCGGAGCCAAAGTCCAACTAAAGGAACTAAAGGAA
Qy 362 TTCAACACAACTATTGACTACCTAAACATCTCTCAAGGAAATAAAATCC
Db 647 TTCAACACAACTATTGACTACCTAAACATCTCTCAAGGAAATAAAATCC
Qy 422 TTGAAGGAGCGCTTATACAGATCTCAAGGAGAGGGGAACTATATA
Db 707 TTGAAGGAGCGCTTATACAGATCTCAAGGAGAGGGGAACTATATA
Qy 482 GTGGGGACGGCCAAACCTTTAGGAATTCCTGGTAAGGGAAAGTACTG
Db 767 GTGGGGACGGCCAAACCTTTAGGAATTCCTGGTAAGGGAAAGTACTG
Qy 542 TAGAAGGCCAAAGATACTTCAAAACAGGGTTTGCAGGCCAACTGAAAGCTGAGA
Db 827 TAGAAGGCCAAAGATACTTCAAAACAGGGTTTGCAGGCCAACTGAAAGCTGAGA
Qy 602 TGCACACAAAAAGCCAGGTTATAATGAGATCCCAAGAGGAGAAATG
Db 887 TGTACACAAAGCTGAGGTTGAGGATGAGGATCCAGAGGAGAAATG
Qy 652 CCTATGGAACTTGGATGAACTGCAAAAGGGGAGATGTTGATGTCA
Db 947 CCTATGGAACTTGGATGAACTGCAAAAGGGGAGATGTTGATGTCA
Qy 722 AGGGCAGCAACGATATCATGGGTAGCTACCAAAATTAAAGGAGGCTCCTGAGA
Db 1007 AGGGCAGCAACGATATCATGGGTAGCTACCAAAATTAAAGGAGGCTCCTGAGA
Qy 782 ACAGAGTGGAGCTGGAGGAAATAATGCTACCAAGGGGAGATGTTGATGTCA

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Db	1067	ACGAGTGTGATGTGGCACGCAAAATGTCGACCAAGGAGGTGAGTTGAGTTTACCCCTC	1126
Qy	842	CTGCACCCCTCAAAAGAGAAAAAGAGAAAAAGAGGAGGCACTAGTCGAGCTGAGTACCACT	901
Db	1127	CTGCACCCCTCAAAAGAGAAAAAGAGAAAAAGAGGAGGCACTAGTCGAGCTGAGTACCACT	1186
Qy	902	ATATGAAATTCCTAAATGGCAAGGGAGTACAGAAAGGGGTAGATCATCTAAATA	961
Db	1187	ATATGAAATTCCTAAATGGCAAGGGAGTACAGAAAGGGGTAGATCATCTAAATA	1245
Qy	962	GGACCAAGCAACCTTAAATGAAAAAACAGGTTCCPAGTAAAGGCAAAAGTCGAGGGCC	1021
Db	1247	GGACCAAGCAACCTTAAATGAAAAAACAGGTTCCPAGTAAAGGCAAAAGTCGAGGGCC	1306
Qy	1022	TGCCCATTCCTCTCGTGTCTGATAATGAAAAAACAGGAAATGGATTCCTTTAATG	1081
Db	1307	TGCCCATTCCTCTCGTGTCTGATAATGAAAAAACAGGAAATGGATTCCTTTAATG	1366
Qy	1082	GCCCCAGTCAGATAAGGATAATAACACATGGCAGAAAATATCATTGTAACAGAC	1141
Db	1367	GCCCCAGTCAGATAAGGATAATAACACATGGCAGAAAATATCATTGTAACAGAC	1426
Qy	1142	AAAATAATTCTACACGGAAATAACGGGTATGCCAACAGGGAAAGGTCCCTGGGTAGACAC	1201
Db	1427	AAAATAATTCTACACGGAAATAACGGGTATGCCAACAGGGAAAGGTCCCTGGGTAGACAC	1486
Qy	1202	CCCATTCACACGGAGGTAGTCCCTGAAGGGATGCAAGTAGTGTAGTCATCTGACA	1261
Db	1487	CCCATTCACACGGAGGTAGTCCCTGAAGGGATGCAAGTAGTGTAGTCATCTGACA	1546
Qy	1262	GTGGCAGTTCAACTGAGGCGATGGTAC	1290
Db	1547	GTGGCAGTTCAACTGAGGCGATGGTAC	1575
Db	290	AAGAGTGTGGTGGGGACTGAGGTGAGTACAGGGACAGAAAGAGAAGAAACTCTCG	349
Qy	238	AATGTTCTAACATAATCCACGAACTGATGAAATTGCTAAAGCACACTCGAACGATATA	297
Db	350	ATGTTCTAACAGGTTAACAGTCCACAGTGTGTCACAAATACTAACACTACAGAGATACA	409
Qy	298	AAGAAGGCTCAAAAGGATTCGGCAAGGAAAGTCCAGTAAAGGAAAGCACCCAT	357
Db	410	GAGAACAAACAGGGCTACTTCAGAACGAGAACACCCCT	469
Qy	358	CGTATTGAAACAAACATCTCCTAAAGTCGAAATAATCCCACTGCT	417
Db	470	CGGGCCGAGAACGGCAACTCCACATCTCCCAATCAGAAAGATCTCTGAGT	529
Qy	418	GATTGTTGAGGAGGCCATTACAGATCTCAAGAGAGGAGGACATGATATACTCTCT	477
Db	530	GACTTCAGGAGACGTGGTCCCAGACCTCTAGTGACGGGGATATTGATGTCCTCTCT	589
Qy	478	TTTCACTGGGGAGGGCAACCCCTTAAGGACATTCCTGTAACAGGAGAGCTACTGTGCT	537
Db	590	TTCACTGGGGAGATGGAAACATTTTATGCAACTCTCCACAGGGAGTGTGAGT	649
Qy	538	GACCTGAAGGAAAAGATAATTCAAAGGGTTGCAAGCCCAGTGTGAGGACT	597
Db	650	GATCCCTGAAACCTCGTGTACCTGTGT--CAGCTCCGAATGTCGAGATGT	706
Qy	598	CATCTTGACACAAAAAGCCAGGTATAATGAGATCCAGAGAGAAATAATGGTGGAA	657
Db	707	GACCCACACAGAATGCTTAATGATGATTCAGGCTCATAGTCATAGGC	766
Qy	658	AATACATTGGAACACTGGATGAAACTGCGTGTGATGTCATGCGCTT	717
Db	767	GGTGCTTATGAAACCAGGAAACACTGGATGAAACTGCGTGTGATGTCATGCGCTT	826
Qy	718	GTAGACGGCACCAACATACTATGGCTAGTACCAATTAGGAGCTCCCTGGAAAGGAGAA	777
Db	827	GTGGGGGAGCAATAAATCAGGGAGTACCAAAATTAGGGAGCTCCCTGGAAAGGAA	886
^Y	778	GGAAACAGACTGGATCTGGCAGGCCAAATGCTCACCAAGGTTGAGTTCTCATAC	837
Db	887	GGAAACAGAGTCGATCCAGGCCAAATGCTCATCAAGGAAAGTGAATTCTACTAC	946
Qy	838	CCTCTGACCCCTAAAGAGAAAAGAGGCGATGTCATGAGCTGAAAGTGTAC	897
Db	947	CCACAAAGGCCCTCAAAAGAGGTTAAAGAGGAGGTAAAGGGCGAGGACACAGGAAGCC	1006
Qy	898	AACATTAATGAAATTCTCTAAATGCTAAAGGCTTCAAGGCAAGGTTCTGAGT	957
Db	1007	GGTTCATGAAATCCTCAAGGAGACCAAGGGGGCTAGCAAGGATGGGAGAATCT	1066
Qy	958	AATAGAAACAGCACCTTAATGAAACAGTTCTAGTAAAGGCCAAAGGTGAG	1017
Db	1067	AAAGGGAAACAGTAACCTGACTGAAAGGGTGTAGATCATCTCT	1137
Qy	1018	GGCTCTGCCATTCCCTCTGCTGATGAAATCAAACGAATGTTGATGTCATG	1126
Db	1127	-----TCTCTCTCACTGCTGTTGATGAGTTAAAGTGGAACTCTCT	1077
Db	1175	AAATGCTCAGTACAGGAGGCTTCAACATGGTAAATGAACTGATGTCATG	1174
Qy	1078	AATGCGCCCTGAGCTGATGAGGAAATAATACATGGAGAAATATATTGTCACCCAC	1137
Qy	1138	AGACAAATAATTCTACCGAACTGGTAAAGGTTGAGTGTGTCATGCT	1254
Db	1214	AGACAAAGCCCTAACGGCTTCTGCTGAGGCTCTGGGCTCTGGCTCG	1273
Qy	1195	AGACAAAGCCATTCAACAGGAGTTAGTCCCTGAGGCTCTGGGCTCTGGCTCG	1254
Db	1274	AGAACGCCCTAACGGCTTCTGAGGCTCTGGCTCTGGGCTCTGGGCTCG	1330
Qy	1255	TCTGACAGTGGCACGAGCTGAGGCTTCAAGTGGAGTCACTGAGT	1314
Qy	178	ATGGGGGCCAGTGTGACTGGGACTGAGTAAACTCTGGGGAAAGGAAAGAACCTTGG	237

Db	1331	TCATCAGTGGAGTCTTAGAGAGGCACTGGACTAGACCCGGGTAGAACAGTT- 1334
Qy	1315	GGTGCAGCTGAAAGACCTCGTACACTGTGAGTTGAGGGACTTC
Db	1390	- - - - - CCCAGCTCT 1398
Qy	1375	TGACCACTGTAAGAGGATAGAGTGGAGAACTGGTGAGCCAGAACTCTGGTCCTT 1434
Db	1399	GTCCTGAGAAAGAGGGACGAGCAGGGACTGAGGTACCAACTGGTACCTC 1458
Qy	1415	GCGGAATTTCGCTATCTTAAATGTCACAGCTATAAAATTCTTAAGGCTTATAGTT 1494
Db	1459	CA-GGACACTGCTGTTAGGGTCTTAAGAACTCCACTAAAGTCTATGCT 1517
Qy	1495	TAAAGCAAAAAATCAATTACAGACCTATGAAATAGGTAACATTGAGTGTCTCAT 1554
Db	1518	TCTGAAATAACTCTGTAAGAATTATAATAATTGTAATATTGACTAGGGCCC 1576
Qy	1555	TAAATAATAGTGGTAGTGTGACAAATGCCCC-TATGTTCTGTAGACATGA 1613
Db	1577	ATTAATAATAGTCGTGATGTGCTTGTGATAGTGTGTTCAAGATGAGATGA 1636
Qy	1614	AATAAACATAATCTCTC 1631
Db	1637	AATAAGGGCTTC 1654
RESULT 8		
	US-09-794-422-3	
	; Sequence 3, Application US/09794422	
	; Publication No. US20030166239A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Brown, Thomas A.	
	; APPLICANT: De Wet, Jeffrey R.	
	; APPLICANT: Gowen, Lori C.	
	; APPLICANT: Hames, Lynn M.	
	; TITLE OF INVENTION: Mammalian Osteoregulins	
	; FILE REFERENCE: PC10445	
	; CURRENT APPLICATION NUMBER: US/09/794,422	
	; CURRENT FILING DATE: 2001-02-27	
	; PRIORITY NUMBER: 60/185,617	
	; PRIORITY FILING DATE: 2000-02-29	
	; PRIORITY APPLICATION NUMBER: 60/234,500	
	; NUMBER OF SEQ ID NOS: 46	
	; SOFTWARE: Patentin Ver. 2.0	
	; SEQ ID NO 3	
	; LENGTH: 1662	
	; TYPE: DNA	
	; ORGANISM: <i>Mus musculus</i>	
	; US-09-794-422-3	
Qy		Query Match 29.3%; Score 485.2; DB 12; Length 1682;
	Best Local Similarity 62.3%; Pred. No. 1,1e-116;	
	Matches 1017; Conservative 0; Mismatches 483; Indels 132; Gaps 11;	
Qy	16	AGTATCAGTAACAAAGAGAACTACTACAATGGCTGAGGATGTCATTATCCTAGTCA 75
Db	166	AGCTGGCCAATCAAGACGATTCAAAAGAACCTGGCAGATCTGTATCTGATTC 225
Qy	76	ACTGGGATAAAGGGTTGAGATGGAGATGCTACATGCAAACTACATGACAGTCGG 195
Db	226	ACGGTGTGATGAGGCCAGAGGATGGCAAGGTCTCTCCCTGACGGCTGGAC 285
Qy	136	GAATATGGCGAGCTCTCATCGAAATAACATGCAAACTACATGACAGTCGG 195
Db		
Qy	196	ATTAATCTCCGGGAGAAAACAAGAGACACCTCTGGAACTGTTCTAAACATAATC 255
Db	346	GGCGAACTACGGAGGGAGGAAACCGAGAGAACCTGAGTCAGTGTCAAGGTAATT 405
Qy	256	CCAGCAAGTATAATTATGCTAAAGGACACTCGAAAGGCTAAAGAGAT 315

406	CCGGCAAGATGTCATGATGCTTAAGTCTCTTAAGACATAAGATAAGAGGTTAT	4.65
316	TCCCCAAGCCAGAAAAGTCCAGTAAAAG-----CAAAGGCCCCATCGTATCAA	3.66
466	CITGTTAACCCAGACAGCCGGTCAAAGGAAAACACACCCCCGAGACCCGAA	5.25
367	CAACATGACTAACATCTCAAAGTCAAAATACTCCAGTGATTTGAA	4.26
526	CGGAGCACTCAACTGACATCTCCACAGATCAAGAGACTCCAGTGACCTTGAA	5.85
427	GGCGCGGTTAACAGATCTCAAGAGAGGGACAAATGATATCTCCCTTCACTGGG	4.86
586	GGCGTGGTCCCAAGATCTCTAGTGGGGAGATAATGTCCTCCCTTCACTGGA	6.45
487	GA CGGC AACCC TTTAAGGACATTCCTGTAAGGAGAGCTACTGTCCTGACCTAGAA	5.46
645	GATGGGACATTTATGACATTCCTGCAAGAAAGG-----ACGTGCTGGTCTGTGAA	7.02
547	GGGAAAGATATTCAACAGCGGTTGAGGCCAAGTGAAGCTGAAAGTACTCATCTGAC	6.06
703	AGCTCAACTAGTGGCC-----CCCTCAAGGCTCCAGCAAGCTGAAAGCTGACACAT	7.59
607	ACAAAAGCCGGTTATGAGATCCAGAGAGAAATGTCGAAATACTATT	6.66
760	ATGAGTGGACTAGCTTAATGAGATCCGGGAGAAGGGACATGTCGAGTGCCTAT	8.19
667	GGRACTGGATGAAACTCGAAAGAGGGAGATGCTGTGATGTCAGCCCTGTAAGGGGC	7.26
820	GCACCCAGAGACAAGCTCAACGGGGAGGCTCTGCAAGGTGGAAGCCTTGTGGGGGC	8.79
727	AGAACCGATATCATGGTAGTACCAATTAAAGAGCTCCCTGAAAGAGGGAAACAGA	7.86
880	AGGAAATGAAATCACAGCAGCCTTCAGGGAACTCCCGGAAAGAGGGAAACAGA	9.39
787	GTCGATGCTGGCAACCAAATGCTCACCAAGGGAGGGTGAAGTTCAATTCCCTCTGCA	8.46
940	ATTAATGGGGAGCAAAATGCTCATCAAGGAAATGAAATTCAAGTGTG	9.99
847	CCCTCAAAAGGAAAAGGAAAGGCACTAGTCATGCACTGAGCTGAAACTATAATT	9.06
1000	GCTCTGAGGAAAGGTAAAGCCGGCTGGAGCATGCA-----GGGAAGGTGGTTAAC	10.56
907	GAATTCTAAATGGCAAGGAGTACAGAAAGGTGATCATTTCTAAATGGAAC	9.66
1057	GAATCCCAAGGGAGGAAAGGTAGCTAGCAAGATGCAAGAGTCCAAAGGAAC	11.16
967	CAAGCACTTAAATGAAAACAAAGGTTCTCGTAGTAAAGGCAAAAGTGAAGGGCTGCC	10.26
1117	CAATTACCTTGACTGGCAAGGAAAGTTCCAGGTAAAGGCAAAAGGCAAGGGCTGTG	11.76
1027	ATTCCTCTCGTGGTCATGATGAAATCAAACGAATGGATTCTTAATGGCCCC	10.86
1177	CTGCCCTCTCACAGTCCTAGTAAAGTGAAGGTTAAAGTGA-----	12.14
1087	AGTCATGAGAATAAACATGGCAAGAAATATCATTATGTAACAGAACAAAT	11.46
1215	-----AGAAGAACATTAATGTTCACTGTCATGGAACAAAT	12.45
1147	AATTCTCACCGAAATAGGGTAGGCCAACAGGAAAGGCTTCCTGGGCT-----AGCAACCC	12.03
1246	AACTCTAACCGAAATAGGGTAGTCACGCCAACGGCTTCCTGCAAGAACCC	13.05
1204	CATTCCACAGGAGGTTAGTTCCTGAGAAGGATGACAGTAGTGAATCTGACACT	12.63
1306	AATTCCACAGCGGGTAGACCCGGAAAG-----AGACAGGAGTTCCTGAGCT	13.62
1264	GGCAGTTCAGTGGACCGATGGTCACTGCACTGGAGGAGTCCAGGGGTGACAGT	13.23
1363	GGGAGTGTCTAGTGGAGTCATGGTGAATGTCAGTGTGACT-----	14.11
1324	CTGAAAGAACCTGTCACCTGTCAGTGTGAGTCACTGGGATTGACAGT-----	13.83

Query Match 2.8%; Score 46.8; DB 12; Length 345;
 Best Local Similarity 46.8%; Pred. No. 0.068; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 92; Other Information: n = A,T,C or G

Db 200 NTTNNNNNGNNNTNNAAAANTTTNNNNNTNNAAANNNTTNTTNAGG 141
 Qy 1603 TGTAGACATGAAAATTAACATCTCTGATGATTAACAAAAAAA 1655
 Db 140 GGGGCAAAATTTTNTNNNNNTNNAGG 88

RESULT 13
 US-10-032-585-6930
 ; Sequence 6930, Application US/10032585
 ; Publication No. US20030180953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Terry, Roemer D.
 ; APPLICANT: Bo, Jiang
 ; APPLICANT: Charles, Boone
 ; APPLICANT: Howard, Bussey
 ; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 ; FILE REFERENCE: 10182-005-999
 ; CURRENT APPLICATION NUMBER: US/10/032,585
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 8000
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 6930
 ; LENGTH: 2826
 ; TYPE: DNA
 ; ORGANISM: Candida albicans

US-10-032-585-6930

Query Match 2.8%; Score 46.6; DB 12; Length 2826;
 Best Local Similarity 51.2%; Pred. No. 0.28; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 104; Other Information: n = A,T,C or G

Db 21 TCTCTTATAATAATAATAATTAGAACACCTTAAATGAAACAAAGCTTCTCTAGTAAGGGCAA 1010
 Qy 951 TCATTCTTAAATGAAACCAAGCAACCTTAAATGAAACAAAGCTTCTCTAGTAAGGGCAA 1010
 Db 21 TCTCTTATAATAATAATAATTAGAACACCTTAAATGAAACAAAGCTTCTCTAGTAAGGGCAA 1010
 Qy 1011 AAGTCAGGGCTCTGCCCATTCCTCTCGTGGTCTTGATAATGAAATCAAACGAATGAA 1070
 Db 81 AATATTGCGATTCATTTGGCTGTGTATATGATTTAATTAATGATAAACAA 140
 Qy 1071 TTCCCTTAATGGGCCAGTCATGAGAAATAATAACATGGGAGAAATAATCATATATG 1130
 Db 141 AACTCATATAAACATACACCTTATATCATACCAATAATTCTGATATACTCATGATG 200
 Qy 1131 ACCCACAGACAAATAATTCTACACGAAATA 1163
 Db 201 AACCACTTACAAAATATTACACCAATAA 233

RESULT 14
 US-09-387-576-831/c
 ; Sequence 831, Application US/09887576
 ; Patent No. US20020144047A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, P.
 ; APPLICANT: Brown, D.
 ; APPLICANT: Chang, H.
 ; APPLICANT: Zhu, T.
 ; APPLICANT: Han, B.
 ; APPLICANT: Wang, X.
 ; APPLICANT: Cooper, Bret
 ; TITLE OF INVENTION: Promoters for regulation of plant expression
 ; FILE REFERENCE: 1360-001US1
 ; CURRENT APPLICATION NUMBER: US/09/887,576
 ; CURRENT FILING DATE: 2001-06-25
 ; PRIORITY APPLICATION NUMBER: US 60/213,848
 ; PRIORITY FILING DATE: 2000-06-23
 ; PRIORITY APPLICATION NUMBER: US 60/214,087
 ; PRIORITY FILING DATE: 2000-06-23
 ; PRIORITY APPLICATION NUMBER: US 60/258,692
 ; PRIORITY FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 875
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0

US-09-353-11753

Query Match 2.8%; Score 46.8; DB 12; Length 345;
 Best Local Similarity 46.8%; Pred. No. 0.068; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 92; Other Information: n = A,T,C or G

Db 1483 GGCTATAATGTTTAAGCAAAATACTTACAGATCTGAAATGGTAACATTTG 1542
 Qy 1483 GGCTATAATGTTTAAGCAAAATACTTACAGATCTGAAATGGTAACATTTG 1542
 Db 260 GGGNNTTTTNTNNNNNTNNAGG 201

Qy 1543 AGTAGGTGTCATTTAAATAAGTGGTCATGTCACAAATGCTCTATGTTGCTC 1602

Search completed: November 29, 2003, 22:35:57
Search time: 642 sec

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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:45:42 ; Search time 21 Seconds (without alignments) 866.365 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 22.9

Sequence: 1 VNKEYSINKENTHGLRMS.....RRDDSSSESDGSSSESDG 430

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/podata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/podata/1/iaa/55_COMB.pep:*

3: /cgn2_6/podata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/podata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/podata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/podata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	140	6.1	772	1	US-09-524-757-12		Sequence 12, Appli
2	135	6.0	1187	1	US-08-559-28		Sequence 28, Appli
3	135	6.0	1187	3	US-08-545-860D-28		Sequence 28, Appli
4	136	6.0	1187	5	PCT-US94-04496-28		Sequence 26, Appli
5	136	6.0	1210	3	US-08-559-26		Sequence 26, Appli
6	136	6.0	1210	3	US-08-545-860D-26		Sequence 26, Appli
7	136	6.0	1210	5	PCT-US94-04496-26		Sequence 26, Appli
8	135.5	5.9	723	1	US-07-814-964-11		Sequence 11, Appli
9	135.5	5.9	723	1	US-08-258-442-11		Sequence 11, Appli
10	135.5	5.9	723	1	US-08-328-809-6		Sequence 6, Appli
11	135.5	5.9	723	4	US-08-866-840-6		Sequence 6, Appli
12	135.5	5.9	723	5	PCT-US92-11107-11		Sequence 11, Appli
13	134.5	5.9	1115	2	US-08-568-459A-2		Sequence 2, Appli
14	134.5	5.9	1115	2	US-08-487-826B-2		Sequence 2, Appli
15	134.5	5.9	1115	4	US-09-210-288-2		Sequence 4, Appli
16	134.5	5.9	1115	6	5198347-6		Patent No. 5198347
17	124.5	5.6	703	3	US-08-910-925-4		Sequence 2, Appli
18	127.5	5.6	1235	1	US-08-118-101A-2		Sequence 2, Appli
19	126.5	5.6	455	5	PCT-US93-07261-13		Sequence 13, Appli
20	126.5	5.6	1663	5	PCT-US93-07261-16		Sequence 16, Appli
21	125.5	5.5	1261	3	US-09-208-742-4		Sequence 4, Appli
22	125.5	5.5	1261	4	US-09-332-295-2		Sequence 2, Appli
23	124.5	5.5	1261	4	US-09-709-979-2		Sequence 2, Appli
24	124.5	5.5	1183	4	US-09-134-001C-3530		Sequence 3510, Appli
25	123	5.4	493	3	US-08-999-774A-12		Sequence 12, Appli
26	123	5.4	1177	4	US-0-134-001C-5106		Sequence 5106, Appli
27	123	5.4	1588	5	PCT-US93-07261-11		Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-524-757-12
; Sequence 12, Application US/08524757
; Patent No. 5792654
; GENERAL INFORMATION:
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Conaway, Joan W.
; APPLICANT: Bradsher, John N.
; TITLE OF INVENTION: RNA Polymerase Transcription Factor
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; CURRENT APPLICATION DATA:
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/524,757
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13621
; FILING DATE: 29-NOV-1994
; APPLICATION NUMBER: US 08/160087
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Harre, John A.
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35006C1PCP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 939-4500
; TELEFAX: (214) 939-4600
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-524-757-12

Query Match 6.1% ; Score 140; DB 1; Length 772;
Best Local Similarity 20.5%; Pred. No. 0.0014;
Matches 87; Conservative 49; Mismatches 144; Indels 144; Gaps 17;

23 PKSTGNKGFFDGGDAISLKHDOEEYGAALIRNNMOHIMGPVTAIKLGEENKENTPRNTVL 82
 :
 210 PGKGSNAFQRLGASQERHLGEPHKGKIVSQNKHEH----- 245
 :
 83 NIIPASMNYYAKAHSKDKKPORDSOAQSPVSKSTHRIOHNIDYLKHLSSKVKLPSDPE 142
 :
 246 ----- KSSHDKRIPVDAKSDEKAASVSRSH----- 277
 :
 14 3 GSGYTYDQLQERDNDISPFSGDQGPFFKDIIGKGEATCPDLEBKDQNGAASPSEARS-THL 201
 :
 278 ----- EENRPPSGDMDAREKP-PSSGVKREKDRGSSLLKKCLPPSEASDNTHL 325
 :
 202 DTKPGYNEIPEREEENGNTGTRDETAKEADAVDVSLLVEGNSNDIM-----GSTNFKEL 255
 :
 Db 326 - KKPGRHD-PEKAK-----LDSKGQJDSFDTG- -KGAGDLIPKVKEGGSINNLKTP 372
 :
 256 PGREGNRVAGDSQNAHOGKV-----EFHYP-----PAPSKEKKEKGSSDAES 298
 :
 Db 373 EGKVKTINLDRKSLGS-LPKVETBDMDFEQQETMSPESYLSDQPKKKKIVKVI-SATA 430
 :
 Qy 299 TNYNEPKRNGSTRKGVDHANRNQATLINEQRFPKGKSGL----- 341
 :
 Db 431 LGDKGLKNNKDSKSTGRNLSDYQKLPKVNTKXSEKPGADALAKLKVDPVLPVLPDPLPA 490
 :
 Qy 342 -----PIPSRGLDNFKNEMDSFNGPSEN-----LITLGERKHYHYP----- 378
 :
 Db 491 IQANYRPLPSLLEISSFQPKRKAFFGTRGRMSRQMVYGSKACYLPKMMT 550
 :
 Qy 379 -HRQ 381
 :
 Db 551 LHQQ 554
 :

 RESULT 2
 US-08-320-559-28
 : Sequence 28, Application US/08320559
 : Patent No. 5633135
 : GENERAL INFORMATION:
 : APPLICANT: Crote, Carlo
 : APPLICANT: Canaani, Eli
 : TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
 : Detection and Treatment of Acute Leukemias
 : TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
 : TITLE OF INVENTION: All-1 Region
 : NUMBER OF SEQUENCES: 44
 : CORRESPONDENCE ADDRESS:
 : STREET: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
 : CITY: One Liberty Place - 46th Floor
 : STATE: Philadelphia
 : COUNTRY: USA
 : ZIP: 19103
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 : COMPUTER: IBM PS/2
 : OPERATING SYSTEM: PC-DOS
 : SOFTWARE: WORDPERFECT 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/320,559
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/062,443
 : FILING DATE: 14 MAY 1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/07/971,094
 : FILING DATE: 30-OCT-92
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/07/888,830
 : FILING DATE: 27-MAY-92
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/07/805,093
 :
 : FILING DATE: 11-DEC-91
 : ATTORNEY/AGENT INFORMATION:
 : NAME: DeLuca, Mark
 : REGISTRATION NUMBER: 33,229
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (215) 568-3100
 : INFORMATION FOR SBQ ID NO: 28:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1187 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-320-559-28
 :
 : Query Match 6.0% ; Score 136, DB 1; Length 1187;
 : Best Local Similarity 20.6%; Pred. No. 0.0038;
 : Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;
 :
 : Qy 92 AKAHSDKDKKPKORDS-----QAQKSPVKSSTH1QHNIDYLKHLSSKVK 135
 :
 : Db 530 SQHESBKDPKSSKAPRAPPAPHPGKRSQCSQPAQEPQPPQQTVGTKQPK-----K 584
 :
 : Qy 136 K1PSDREGSGYTDLQERGNDNDISPSGDGPQFKD1P-----GRGE-----ATGPDL 181
 :
 : Db 585 PVKASARASGRTSLSQEREPOLPLPSRQDQTSDKPKVTKGRPAAASNEPKPAVPPSS 644
 :
 : Qy 182 EGKDIOTGFAGPSEAS-----THLDTKKKPGY-----NEIPEREEENGNTGTRDE 227
 :
 : Db 645 EKKKHKSSLPAPSALSGPBPADKNDVDEDRTEPHFALVPLTESQGPBPHGSSRTSGCRA 704
 :
 : Qy 228 TAKEADAVDVSLLVEGNSNDINGSTNPKELPGREGNEY-----DASSQNAHSGKVE 276
 :
 : Db 705 VVQEQNSKURKLPLRDTKYLSPLRDTPPFQSLMVKITLDSLRTIPQPPGKGSQRKAE 764
 :
 : Qy 277 FHYPPAPSKERKEGSSDAEESTNNNE1PKNGKGGSTRKGVDHSNNRNQATUNEKORFPSKG 336
 :
 : Db 765 DKQPAGKHSSEKERSSDSS-----SKLAKKRKGEAERDCD-----NKKIR----- 805
 :
 : Qy 337 KSQLGLPISPLRSRGLDNETKNEMDSENGPSENIT-----HGRKYHYPHRNNNSTRNK 388
 :
 : Db 806 -----LEKEIKSOSSSSSSHKESSKTPSRPSSQSSKEMLPPPPVSSSQKQ 854
 :
 : Qy 389 GMPQKGS-----WGRQ-----HSNRFSSRRDDSSSSSGSSSE-----SDGD 430
 :
 : Db 855 AKPALKRSRREADTCQDPPKSASSSTKSNHKDSS1PKQRRVEGKGSRSSEHKGSSGD 912
 :
 : RESULT 3
 : US-08-545-860D-28
 : Sequence 28, Application US/08545860D
 : Patent No. 6040140
 : GENERAL INFORMATION:
 : APPLICANT: Crote, Carlo
 : APPLICANT: Canaani, Eli
 : TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 : for Detection and Treatment of Acute Leukemias
 : TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
 : NUMBER OF SEQUENCES: 94
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
 : ADDRESS: No. 6040140ris
 : STREET: One Liberty Place, 46th Floor
 : CITY: Philadelphia
 : STATE: Pennsylvania
 : COUNTRY: USA
 : ZIP: 19103
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/545,860D
 FILING DATE: 07-MAR-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE: 22-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10930
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/327,392
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/320,559
 FILING DATE: 11-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/062,443
 FILING DATE: 14-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/971,094
 FILING DATE: 30-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,839
 FILING DATE: 27-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/805,093
 FILING DATE: 11-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Deluca Esq., Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE DOCKET NUMBER: TJO-1262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-4349
 INFORMATION FOR SEO ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 -08-545-860D-28

RESULT 4
PCT-US94-04496-28
Sequence 28, Application PC/TUSS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Cannani, Elio
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
ADDRESS: Norris
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-04496-28

Query Match 6.0%; Score 136; DB 5; Length 1187;
Best Local Similarity 20.6%; Pred. No. 0.058;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 1

92 AKAHSDKKKQDSDS-----OQKSPVSKSKTRIQHNIDYLKLHSVK 13
530 SQEHESSKIDPPKSSKAPRAPPAPHGKRSCQKSQPKQQEPQQRTQVTKQPK-----K 58

136 KIPSDPFGSGTYTDLQERGNDNTSPFGSDGQPFKIDIP--GKGE-----ATGPDL 18

585 PVKASARAGSRTSILQGERPGLPYSRQDTSKDKPRTKGRPRAASNEPKAVPPSS 64

182 EGGDIDTGFQGPSEAES-----THLDTTKPGY-----NEIPEREEGGNTTGTTRDE 224

645 EKKRKHSPLPAPSKAISGPPEAKDNDVDEDRTPHEFALYVPLTESQPPHSSGSRSGRQ 704

228 TAKEADAVDVSLEGVSESDIMGSTNFKEPLGRGGRV-----DAGSONNHQGKVE 270
705 VVQDSDSKRDLPLPLARDTKELSPLRDTPPPSLMVKITLDLISRIPQPPGKGSQRQKAE 766

277 FHYPPAPSKEKREKKESSDAASSTNTAEBIPKNGKSTRKGVDHSNRNQATLNERKQRFPSK 331
765 DKQPAAGKCHSSKEKSSDSS-----SKLAKKRGGEAERDCD-----NKKTR-----805

337 KSQGLPISPGKLDNNEIKNEMDSFGNPGSHENLIT-----HGRKYHYVPHRONSTRNK 385
806 -----LEKEIKSQQSSSSSSSHKESSKTPSPSSQSKKEMLPQPPVSSSSQKRP 855

RESULT 5

Qy 389 GMPOQKGS ----- WGRQP ----- HSRRFSSRRDDSESSSGSSESE ----- SDGD 430
Db 855 AKPALKRSRREADTCGDPKSSASSTKSNHKDSSTPKQRRVEGKCSRSSSEHKGSSGD 912

US-08-320-559-26

Sequence 26, Application US/08320559

GENERAL INFORMATION:
Patent No. 5633135

APPLICANT: Croce, Carlo
Canaani, Eli

TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
Detection of Acute Leukemias

TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the
Title of Invention: All-1 Region

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COUNTRY: USA

RESULT 6

US-08-545-860D-26

Sequence 26, Application US/08545860D

GENERAL INFORMATION:
Patent No. 6040140

APPLICANT: Croce, Carlo
Canaani, Eli

TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
for Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the All-1

SEQUENCE LENGTH: 1366

SEQUENCE ID: 1

SEQUENCE:

668 EKKHKSLLPAPSKAALGPEAPDADVEEDRTPPHFALVPLTESGGPPHSGSGSTSGCQA 727
228 TAKEADAVDLSLVEGSNDIMGSTNFKELPGRGNGRV ----- DAGSQNAHOGKVE 276
Db 728 VVYQEDSRKDRKPLPLRDTKJLSPRTRPPPSLMSVKITLDLISRIPQPPGKSRORRAE 787
277 FHYPPAPSKEKRGSSDAESTNYNEIPKNGKSTRGVGDHSNRQATLNEQRQFPSKG 336
Db 788 DKOPPACKHASSERSDSS ----- SKLAKRKGABRDCD ----- NKKIR ----- 828
337 KSQLLPPIPSRGLDNRKNEMDNSFGPSENIT ----- HGRKTHYVPHQNNSTENK 388
Qy 829 ----- LEKETKSQQSSSSSHKESSSTKPSRSPSSQSKEMLPPPPVSSSSQKRP 877
389 GMPQGKGS ----- WGRQP ----- HSNRRSSSSRDDSSSSDSSSE ----- SDGD 430
Db 878 AKPAKXBSRREADTCGDPKPSASSTKSNHKDSSTPQRRVKGKSSSSBEHKGSSGD 935

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE: 14 MAY 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-4339
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-320-559-26

Query Match 6.0%: Score 136; DB 1; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0059; Mismatches 52; Indels 114; Gaps 14;
Matches 86; Conservative 52;

Qy 92 AKANISDKKKKKQQRDS----- QAQKSPVKSSTHRQHNDYLKHLSKYK 135
Db 553 SQESESKUPPKSSSKAARAPPELPHPGRSQCKSPQAQBPQRTQVTKQPK ----- K 607
136 KIPSPDEGGGTYTDIQRGNDISPSFGDGQPFKDIP ----- GKGE ----- ATGPDI 181
Qy 608 PVKASARAASRTSLQERFGLLPGSRDQTSKDKPKVTKGRPRAASNEPKAVPPS 667
182 EGKQ1QTGAGPSEARS ----- THLDTKKPGY ----- NEIPERENGNTGTRDE 227

Qy

NAME: DeLuca Esq., Mark
 REGISTRATION NUMBER: 3,229
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-545-360D-26

Query Match 6.0% Score 136; DB 3; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.059;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

Qy 92 AKAHSKDKKKPQRDS-----QAQKSPVKSSTKTHRIQHNDYLKHLISKVK 135
 Db 553 SQHSESKDPPPKSSKAPRAPPEAPHGKRSQSKPQAQPQPQRQTYGTRQPK-----K 607

Qy 92 AKAHSKDKKKPQRDS-----QAQKSPVKSSTKTHRIQHNDYLKHLISKVK 135
 Db 553 SQHSESKDPPPKSSKAPRAPPEAPHGKRSQSKPQAQPQPQRQTYGTRQPK-----K 607

Qy 136 KTPSDFEGCGYTDLQERGNDISPPSGDGQPFKDIP-----GKGB-----ATGPDL 181
 Db 608 PYKASARAGSRSTSLSQGERGPGILIPYGRSDQTSDKPKVTKGRPRAASNEPKPAVPPSS 667

Qy 182 EGKDIQPGFAGPSEAES-----THLDTKPGY-----NEIPEREEENGANTIGTRDE 227
 Db 668 EKKKHSLLPASKALSGPEAKDNEDTPHFAHVPLTESQGPSPHSGGRTSGRQA 727

Qy 228 TAKEADAVDVSIVEGNDIMGSTNFKBLPGREGRNRY-----DAGSQNAHOGKVE 276
 Db 728 VVQEDSRKDRLPLPLRDTKLLSPRDTPPSLSMVKITDILSRIFQPPGKGSRORKAE 787

Qy 277 FHYPPAPSKEKKEGGSDAAETTNYNEIPIKNGKGSPRKGVDHSNRNRQATLIEKORPSKG 336
 Db 788 DKQPPACKKHSEBKRSDDSS-----SKLAKRKGEAERDCD-----NKKIR-----828

Qy 337 KSGQGLP1PSRGILDNEIKNEMDSFNGPSHENIT-----HGRKTHYVPHQRQNNSTRNK 388
 Db 829 -----LEKEIKSQQSSSSSSHKESSKTKPSPRSSKKMPLPPVSSSSQKQ 877

Qy 389 GMPQGKGS-----WGRQP-----HSNRPFSRRDDSSSDGSSSE---SDGD 430
 Db 878 AKPALKRSRREADTCGDPKSSASSTKSNHKDSSIPKQRVEKGKSRSSSBHKGSSGD 935

RESUL 7 PCT-US94-04496-26

Sequence 26. APPLICATION PC/TUSS9404496
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 INVENTOR: Carraani, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Norris
 STREET: One Liberty Place. 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:

RESULT 8 US-07-814-964-11
 Sequence 11. Application US/07814964
 Patent No. 559047
 GENERAL INFORMATION:
 APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Lippard, Stephen J.
 APPLICANT: Bill, Peter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellelt, Patri
 APPLICANT: Bessigmann, John M.
 APPLICANT: Lippard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/814,964
 FILING DATE: 19911226
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-851-9540
 INFORMATION FOR SEQ ID NO: 11
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: AMINO ACID
 TOPOLGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP (predicted)
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 458..507
 OTHER INFORMATION: /label= Acidic
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 518..547
 OTHER INFORMATION: /label= Basic I
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 547..620
 OTHER INFORMATION: /label= HMG-box
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 632..649
 OTHER INFORMATION: /label= Basic II
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 557..723
 OTHER INFORMATION: /label= Mixed Charge
 US-07-814-964-11

Query Match 5.9%; Score 135.5; DB 1; Length 723;
 Best Local Similarity 23.2%; Pred. No. 0 0032;
 Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLK---GSKYKIPSPFEGSGYTDLQERGNDIDSPSGDQGPFDQPG-KGEATGPD 180
 Db 416 DYTQKLUVSNNGK---DKSSEKDV-DFGSD---NNEPDAYLARUKAAREKE 464

QY 181 LEGKDIQTFAGPSEAESTHLDYKPGYNEIPEERENGNTGTRDETAKEADAVDSL 240
 Db 465 EDDDD---GDSDEESTDEFK-KPNENESDAEYDSNEVSDDD---DSDASG--- 510

QY 241 EGNDIMGSTNFKELPGREGNRVDAQSNAHQGRKVETPFYPPAPSKEKREGS---- 292
 Db 511 -GGGDSGAKKKKEKKSEKKEKKEKERTK---KPSKKKKDSGPKRATTA 562

QY 293 ---SDAEE-----TNYNEIPKNGKSTRKGVDHSNRNQATLNEKORFSPSKGKSQGL 341
 Db 563 MLWLNDRPESIKRBNPGLKVTETAKKGSEMWKLKDQSKWEDAAKDQRY----- 613

QY 342 PIPSRGLDNEIKNEMDSFNGPSHENITIITGRKYHYVPHRQNINSTRNKGMPQKGWSGR- 399

Db 614 -----HDEMNYKPEAGGDSNEKG--GKSSKKRKT 642
 QY 400 QPHSNRR-----FSSR--RDDSSESSDSGSSSE-----SDGD 430
 Db 643 EPSPSKKANTSGFKSKEYISDDDSDEKNEPAKKSKFPPSDGD 691

RESULT 9
 US-08-258-442-11
 Sequence 11, Application US/08258442
 Patent No. 5670621
 GENERAL INFORMATION:
 APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Brunn, Suzanne L.
 APPLICANT: Pill, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellelt, Pati
 APPLICANT: Essigmann, John M.
 APPLICANT: Lippard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 TITLE OF INVENTION: Protein and Uses Therefor
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEER: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Millett Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/258,442
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-478/AA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE: Drosophila melanogaster
 IMMEDIATE SOURCE: Drosophila SSRP (predicted)
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 458..507
 OTHER INFORMATION: /label= Acidic
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 518..547
 OTHER INFORMATION: /label= Basic I
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 547..620
 OTHER INFORMATION: /label= HMG-box
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 632..649
 OTHER INFORMATION: /label= Basic II
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 557..723
 OTHER INFORMATION: /label= Mixed Charge
 US-08-258-442-11

Query Match 5.9%; Score 135.5; DB 1; Length 723;
 Best Local Similarity 23.2%; Pred. No. 0 0032;
 Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLK---GSKYKIPSPFEGSGYTDLQERGNDIDSPSGDQGPFDQPG-KGEATGPD 180
 Db 416 DYTQKLUVSNNGK---DKSSEKDV-DFGSD---NNEPDAYLARUKAAREKE 464

QY 181 LEGKDIQTFAGPSEAESTHLDYKPGYNEIPEERENGNTGTRDETAKEADAVDSL 240
 Db 465 EDDDD---GDSDEESTDEFK-KPNENESDAEYDSNEVSDDD---DSDASG--- 510

QY 241 EGNDIMGSTNFKELPGREGNRVDAQSNAHQGRKVETPFYPPAPSKEKREGS---- 292
 Db 511 -GGGDSGAKKKKEKKSEKKEKERTK---KPSKKKKDSGPKRATTA 562

QY 293 ---SDAEE-----TNYNEIPKNGKSTRKGVDHSNRNQATLNEKORFSPSKGKSQGL 341
 Db 563 MLWLNDRPESIKRBNPGLKVTETAKKGSEMWKLKDQSKWEDAAKDQRY----- 613

QY 342 PIPSRGLDNEIKNEMDSFNGPSHENITIITGRKYHYVPHRQNINSTRNKGMPQKGWSGR- 399


```

OTHER INFORMATION: /label= Acidic
FEATURE: Domain
NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label= Basic I
FEATURE: Domain
NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION: /label= HMG-box
FEATURE: Domain
NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION: /label= Basic II
FEATURE: Domain
NAME/KEY: Domain
LOCATION: 657..723
OTHER INFORMATION: /label= Mixed charge
PCT-US92-111-07-11

Query Match Score 135.; DB 5; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0032;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;
Qy 126 DYLK---HLSKYKIPSPREGSGXTDLOERGNDNISPPSGDQPFKDIPG-KGREATGPD 180
Db 416 DYTQKKEHUVSNNGK---DKSGXKDV-DFGDS---NENE DAYLARLKAFAREKE 464
Qy 181 LEGKDIQTFGAGPSEABSTHLDTKPGYBIPEREEGGNTIGPRDETAKEADAVDSL 240
Db 465 EDDDD---GDSDEETDDEDF KPNNNEESDVAEYDSNVESSDD---DSDASG--- 510
Qy 241 EGSDNDIMGSTTNFKELPGREGNRVDAQGKVEYHPPAPPSKEXKRGES----- 292
Db 511 -GGGDSGAKKKEKKKSKKEKKKEKERTK-----KPSKKKRDGSKPKRATTAF 562
Qy 293 ----SDAEE-----TNYNEIPKNGKSTRGVDHSNRNOATLNEKORFPSKGKSQJL 341
Db 563 MLWLNDFRESIKRNPGLKVTEAKKGEMMWKLKDQSWEDAALKDQRY----- 613
Qy 342 PIPSRGLDNEITKNEMDSSNGPSPHENIITHGRKYHYPHRQNSNSTRNKGMDQGKGSWGR-- 399
Db 614 -----HDEMKRYKPEAGGDSDNEKG---GKSSKKRKT 642
Qy 400 QPHSNRR-----FSSTR--RDDSSESSSDSGSSSE-----SDGD 430
Db 643 EPSPSKRANTSGSGFKSKEYISDDSTSSDDEKDNEPAKKKSKPPSDGD 691

RESULT 13
US 08-568-459A-2
; Sequence 2, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/568,459A
 FILING DATE: 07-DEC-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned
 REGISTRATION NUMBER: 29,655
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: NIH121.001CP1
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1115 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGIN/ SOURCE:
 ORGANISM: Plasmodium vivax
 8-568-459A-2

Query Match 5.9%; Score 134.5; DB 2; Length 1115;
 1st Local Similarity 20.0%; Pred. No. 0.0071; Gaps 21;
 Itches 97; Conservative 80; Mismatches 220;

2 NKEYSISNKENTINGLMSIYPKSTGNKGPEGDDAIKSLHQEEYGAIRNMQHIMG 61
 500 NKFVSKVNAEAKVQTAGIVTPY-----DILHQ-EELDFNEVAFENEINKRDG 544

62 PVAIAKLLG-BENKENTPRVNLIIPASMYNAKASHQKPKORDSQOKSPVKSSTHR 120
 545 AYIELCVCSVEEAKNTQEVVTVNDAAKSOA-TNSNP1SQPVDSKRAEKVP-GDSTH 600

121 IQRHIDYKRLHSKV-KKIPSDFFGSGTQFLDQ--ERGNDNDISPGSDGQFQPKGKB- 175
 601 -GRNVNSGODSSSTGKAVTGDGNGNQTPAEDSVQRSDIAESYSARNDVQPKSVRSRSD 658

176 ---ATGPDELEGDQTQTFAGPSRAESTHLDTKPKP-----YNEI 211
 659 TASVYGGIAEAGKE-NLGASNRSRESETEV-VEANSPGDDTVNSAS1IPVYVGENPLVTPYNG 716

212 PEREENGPN-----TIGTRDTEKAEADAVDVSILVEGNSNDIMGSTNFKEBLPGRBGN 261
 717 RHEKDNDSIDGPAESMANPDNSNSKGEIGKGQONDMAKATKDSSNSDGT-----SATGD 771

262 RVDAGSONAHOGKVEHYPPAPSKERKEKKEKGSS--DAEESTNNE1PKNGKGST--RKG 315
 772 TTDVDRDPIKGVPEDRDKTVGSSKDGGEDEDSANKDAATVVGEDRIRENSAGGSTDNSRK 831

316 VDHSNRNGDATLNEKQR--FPGSKGSKQH1PIPSRG-LDNE1KNEMDSPNGPSHEN1THG 371
 832 NDTEKNGASTPDKQSEDATLSKTSLESSTBSGDRTNDTNSLENGNGKEKDLQRKHD 891

372 RKHYHYPHRQNSTR-----NKGKMPQGKCSWGRQPHSNR-RFSSRRDSDSESSSDSG 422
 892 FKSNDTPKEEPNSDQTTDAEGHDRDS1KNDKAE--RKKHMKDFTKNTNSHHLNSNNL 949

423 SSSSESD 428
 950 SNGKLD 955

APPLICANT: Peterson, David S.
 / APPLICANT: Su, Xin zhuan
 / APPLICANT: Willems, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: AND PLASMODIUM FALCIPIARUM ERYTHROCYTE BINDING PROTEINS
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487, 826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsson, Ned
 REGISTRATION NUMBER: 29, 655
 REFERENCE/DOCKET NUMBER: NIH121.001CP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-0176
 TELEFAX: (619) 235-8550
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1115 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Plasmodium vivax
 US-08-487-826B-2

Query Match 5 9%; Score 134.5; DB 2; Length 1115;
 Best Local Similarity 20.9%; Pred. No. 0.0071;
 Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;

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Qy	62	PVTAALKLG-BENKENTPRAVLNLTIPASMYAKHSRKKKPQDQSQQSKP	VSKPSKTHR	120	
Db	545	YIYELCVCSVEAKNTQEVVNTVDNAASQSA-TNSNPISQPVDSKAKV	P-KV-	GDTSH-	600
Qy	121	IQHNTDYLKHLKSV-KRIPSDFEGGGTDLQ--	-ERGNDIDSPSGDQPFKDIPGKCB-	175	
Db	601	-GNTVNGQDSSTICKAVTGDGONGNQTAESDVQSDIAESVAKNDPQKVSKSDD	-	658	
Qy	176	--ATCPDLEKGKDQTGFAGPSEAESLHDLTKKG-	-	-YNEI 211	
Db	659	TASVIGIAEAGKE-NLGASNRSRPSST-	-	-	
Qy	212	PEREENGGN-----TIGRDTETAKADAVSLSVEGSDIMGTSNFKELPGBEGN	-	261	
Db	717	RHSNSDSDGPAESMANPDSNSKATGQDNDMATAKTDSSNSDCTS-----	-	SATGD 771	
Qy	262	RVDAGSQNAHQKGYEFHYPPAPSKERKEGSS--	-DAAEESTNNEIPKNGKGS	315	
Db	772	TTDAVTRTENKGVPDRTKVGSDGGEDNSANKDAATVGDRIENSAGGSTMRSK	-	831	
Qy	316	VDHSNRNQATLNEKOR--FFSKGKSQGLP1PSRG--LDENEKHMEDSENGPSENHILTHG	371		
Db	832	NDTBNKAGASTPDSKOSDATAKSLESTESDRTNDTNSLENGGKEKDLOKHD	-	891	

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Qy 176 --ATGPDLEGKDIOTGFAGPSEAESTHLDTRKPG----- YNEI 211
Db 659 TASVIGAEGAGE-NLGASNSPSEST-VEANSPGDTVNSA S1PVVSGTENLVTPTNGL 716
Qy 212 PEREENGNN-----TIGTRDETAKEADAVDVSLEVGNSNDIMGSTNFELPGREGN 261
Db 717 RHSKDNDSDGPAESMANPDSNSKGGETKGQNDMAKATKDSSNSDCTS----SATGD 771
Qy 262 RVDAGSQNAHQKQVEFHYPAPSKERKKGSS--DAAESTVNNIEIPKGKST-- RKG 315
Db 772 TTDADVDRINKSPEDRDKTVSSKGCGEDNSANKDAATVVGEBDRIRENSAGGSTNDRSK 831
Qy 316 VDHSNRQATUNEBQR - FPSKGKSQGLPIPSRG--LDNEIKNMDSFNGPSHENITHG 371
Db 832 NDTEKNGASTPSKQSEDATANSKTESLESTSGDRITNDTINSLENKGKGERDLOKHID 891
Qy 372 RKYHYVPHRONNSTR-----NKGMFQKGSSWGRPHSNR-RFSSRRDSSSESSDSG 422
Qy 892 FKSNDTPNEEPNSDQTTDAEHDRTS1XNDKAE - RRKHMNDTFTKNTSHLNSNNL 949
Qy 423 SSSESD 428
Db 950 SNGKLD 955

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Search completed: November 26, 2003, 15:49:09
 Job time : 23 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2276	99.9	509	12	US-09-794-422-34	Sequence 34, Appli	Sequence 27, APP1
2	2276	99.9	525	12	US-09-794-422-6	Sequence 6, Appli	Sequence 8, APP1
3	2276	99.9	525	12	US-09-311-840-1	Sequence 1, Appli	Sequence 24, APP1
4	2276	99.9	540	12	US-09-794-422-46	Sequence 46, Appli	Sequence 32, APP1
5	2276	99.9	556	12	US-09-794-422-8	Sequence 8, Appli	Sequence 7, APP1
6	2269	99.6	525	10	US-09-814-550-2	Sequence 2, Appli	Sequence 10, APP1
7	983.5	43.2	441	12	US-09-794-422-4	Sequence 4, Appli	Sequence 25, APP1
8	938	41.2	435	12	US-09-794-422-4	Sequence 4, Appli	Sequence 28, APP1
9	514	22.6	97	10	US-09-812-485A-1	Sequence 2, Appli	Sequence 30, APP1
10	246	10.8	47	10	US-09-812-485A-2	Sequence 1, Appli	Sequence 17, APP1
11	235.5	10.3	47	10	US-09-812-485A-3	Sequence 2, Appli	Sequence 16, APP1
12	229	10.0	47	10	US-09-812-485A-4	Sequence 3, Appli	Sequence 29, APP1
13	218	9.6	40	10	US-09-812-485A-23	Sequence 23, Appli	Sequence 31, APP1
14	216	9.5	44	10	US-09-812-485A-6	Sequence 6, Appli	Sequence 33, APP1
15	215	9.4	44	10	US-09-812-485A-5	Sequence 5, Appli	Sequence 35, APP1
16	214.5	9.4	45	10	US-09-812-485A-27	Sequence 2, Appli	Sequence 37, APP1
17	198.5	8.7	41	10	US-09-812-485A-8	Sequence 2, Appli	Sequence 39, APP1
18	190.5	8.4	40	10	US-09-812-485A-24	Sequence 2, Appli	Sequence 41, APP1
19	188.5	8.3	37	10	US-09-812-485A-32	Sequence 2, Appli	Sequence 43, APP1
20	182	8.0	37	10	US-09-812-485A-7	Sequence 2, Appli	Sequence 45, APP1
21	180	7.9	38	10	US-09-812-485A-10	Sequence 2, Appli	Sequence 47, APP1
22	163.5	7.2	35	10	US-09-812-485A-25	Sequence 2, Appli	Sequence 49, APP1
23	157.5	6.9	35	10	US-09-812-485A-28	Sequence 2, Appli	Sequence 51, APP1
24	153.5	6.7	33	10	US-09-812-485A-10	Sequence 2, Appli	Sequence 53, APP1
25	152	6.7	1253	12	US-10-362-798-2	Sequence 2, Appli	Sequence 55, APP1
26	150	6.6	32	10	US-09-812-485A-12	Sequence 2, Appli	Sequence 57, APP1
27	148	6.5	1884	10	US-09-785-770A-17	Sequence 2, Appli	Sequence 59, APP1
28	148	6.5	1907	10	US-09-785-770A-16	Sequence 2, Appli	Sequence 61, APP1
29	146.5	6.4	33	10	US-09-812-485A-31	Sequence 2, Appli	Sequence 63, APP1
30	146	6.4	2174	12	US-10-087-887-87	Sequence 2, Appli	Sequence 65, APP1
31	144.5	6.3	665	11	US-09-820-843A-107	Sequence 2, Appli	Sequence 67, APP1
32	142.5	6.3	351	10	US-09-812-485A-12	Sequence 2, Appli	Sequence 69, APP1
33	142.5	6.3	31	10	US-09-812-485A-33	Sequence 2, Appli	Sequence 71, APP1
34	140	6.1	772	15	US-10-153-668-02	Sequence 2, Appli	Sequence 73, APP1
35	137.5	6.0	30	10	US-09-812-485A-26	Sequence 2, Appli	Sequence 75, APP1
36	136	6.0	1210	15	US-10-205-823-564	Sequence 2, Appli	Sequence 77, APP1
37	134.5	5.9	1115	14	US-10-153-273-2	Sequence 2, Appli	Sequence 79, APP1
38	133.5	5.9	1462	12	US-10-287-218-7	Sequence 2, Appli	Sequence 81, APP1
39	131.5	5.8	2476	11	US-09-24-574-7	Sequence 2, Appli	Sequence 83, APP1
40	129.5	5.7	370	10	US-09-812-485A-29	Sequence 2, Appli	Sequence 85, APP1
41	129.5	5.7	677	15	US-10-060-036-4552	Sequence 2, Appli	Sequence 87, APP1
42	129	5.7	28	10	US-09-812-485A-14	Sequence 2, Appli	Sequence 89, APP1
43	127	5.6	322	11	US-09-747-660A-64	Sequence 2, Appli	Sequence 91, APP1
44	127	5.6	718	10	US-09-738-626-5661	Sequence 2, Appli	Sequence 93, APP1
45	127	5.6	1365	11	US-09-884-465A-382	Sequence 2, Appli	Sequence 95, APP1

ALIGNMENTS

RESULT 1
US-09-794-422-34
Sequence 34, Application US/09734422
; Publication No. US20030166339A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Haines, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; PCT REFERENCE: PCT/04/5
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIORITY APPLICATION NUMBER: 60/185,617
; PRIORITY FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-34
Query Match 99.9%; Score 2276; DB 12; Length 509;
Best Local Similarity 99.8%; Pred. No. 4.3e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 VNKYESISNKENTHNGLMSIYPKSTGNKGFEQDGDALKLHQEYGAALIRNNQHIM 60
; : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2276	99.9	509	12	US-09-794-422-34	Sequence 34, Appli	Sequence 27, APP1
2	2276	99.9	525	12	US-09-794-422-6	Sequence 6, Appli	Sequence 8, APP1
3	2276	99.9	525	12	US-09-311-840-1	Sequence 1, Appli	Sequence 24, APP1
4	2276	99.9	540	12	US-09-794-422-46	Sequence 46, Appli	Sequence 32, APP1
5	2276	99.9	556	12	US-09-794-422-8	Sequence 8, Appli	Sequence 7, APP1
6	2269	99.6	525	10	US-09-814-550-2	Sequence 2, Appli	Sequence 10, APP1
7	983.5	43.2	441	12	US-09-794-422-4	Sequence 4, Appli	Sequence 35, APP1
8	938	41.2	435	12	US-09-794-422-4	Sequence 4, Appli	Sequence 37, APP1
9	514	22.6	97	10	US-09-812-485A-1	Sequence 2, Appli	Sequence 39, APP1
10	246	10.8	47	10	US-09-812-485A-2	Sequence 2, Appli	Sequence 41, APP1
11	235.5	10.3	47	10	US-09-812-485A-3	Sequence 4, Appli	Sequence 43, APP1
12	229	10.0	47	10	US-09-812-485A-4	Sequence 3, Appli	Sequence 45, APP1
13	218	9.6	40	10	US-09-812-485A-23	Sequence 23, Appli	Sequence 47, APP1
14	216	9.5	44	10	US-09-812-485A-6	Sequence 6, Appli	Sequence 49, APP1
15	215	9.4	44	10	US-09-812-485A-5	Sequence 5, Appli	Sequence 51, APP1

Db 200 IQHNDYLKHLKVKKIPSEFGSVDLQERGNDISPGDGQPRKD1PGKBEATGPD 259
 Qy 181 LEGKDIQTFGPSEASLTHLDTKKGYNEPEREEENGNTIGTRDETAKEADAVDVLV 240
 Db 260 LEGKDIQTFGPSEASLTHLDTKKGYNEPEREEENGNTIGTRDETAKEADAVDVLV 319
 Qy 241 EGSNDIMGSTNFKELPGREGNRVDAAGTQPSKKEKRKEGSSDAESTN 300
 Db 320 EGSNDIMGSTNFKELPGREGNRVDAAGTQPSKKEKRKEGSSDAESTN 379
 Qy 301 YNEIPKNGKGSTRGYDHSNRNQATLNKEQKRPFSKCKSQGLPISRGDNEIKNEMDSFN 360
 Db 380 YNEIPKNGKGSTRGYDHSNRNQATLNKEQKRPFSKCKSQGLPISRGDNEIKNEMDSFN 439
 Db 361 GPSHENITTHGRKYHYVPHRQNNSTRANKGMPQGKGSWGRPHSNRFSRRDDSSBSSD 420
 Qy 440 GPSHENITTHGRKYHYVPHRQNNSTRANKGMPQGKGSWGRPHSNRFSRRDDSSBSSD 499
 Qy 421 SGSSSESDGD 430
 Db 516 SGSSSESDGD 525

RESULT 3
 US-10-311-840-1
 ; Sequence 1, Application US/10311840
 ; Publication No. US20030175808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUROKAWA, Tomofumi
 ; APPLICANT: YAMADA, Takao
 ; APPLICANT: MORIZOTO, Shigeto
 ; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
 ; FILE REFERENCE: 2738010P
 ; CURRENT APPLICATION NUMBER: US/10/311,840
 ; CURRENT FILING DATE: 2003-12-18
 ; PRIORITY NUMBER: PCT/JP01/05263
 ; PRIORITY PILING DATE: 2001-06-20
 ; PRIORITY APPLICATION NUMBER: JP 2000-191088
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 1
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-311-840-1

Query Match 99.9%; Score 2276; DB 12; Length 525;
 Best Local Similarity 99.8%; Pred. No. 4.5e-173;
 Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 60
 Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 155
 Qy 61 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 120
 Db 156 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 215
 Qy 121 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 180
 Db 216 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 275
 Qy 181 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 240
 Db 276 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 335
 Qy 241 EGSNDIMGSTNFKELPGREGNRVDAAGTQPSKKEKRKEGSSDAESTN 300
 Db 336 EGSNDIMGSTNFKELPGREGNRVDAAGTQPSKKEKRKEGSSDAESTN 395
 Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 60
 Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 155
 Qy 61 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 120
 Db 156 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 215
 Qy 121 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 180
 Db 216 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 275
 Qy 181 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 240
 Db 276 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 335
 Qy 301 YNEIPKNGKGSTRGYDHSNRNQATLNKEQKRPFSKCKSQGLPISRGDNEIKNEMDSFN 360
 Db 396 YNEIPKNGKGSTRGYDHSNRNQATLNKEQKRPFSKCKSQGLPISRGDNEIKNEMDSFN 455
 Qy 361 GPSHENITTHGRKYHYVPHRQNNSTRANKGMPQGKGSWGRPHSNRFSRRDDSSBSSD 420
 Db 456 GPSHENITTHGRKYHYVPHRQNNSTRANKGMPQGKGSWGRPHSNRFSRRDDSSBSSD 515
 Qy 421 SGSSSESDGD 430
 Db 516 SGSSSESDGD 525

RESULT 3
 US-10-311-840-1
 ; Sequence 1, Application US/10311840
 ; Publication No. US20030175808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUROKAWA, Tomofumi
 ; APPLICANT: YAMADA, Takao
 ; APPLICANT: MORIZOTO, Shigeto
 ; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
 ; FILE REFERENCE: 2738010P
 ; CURRENT APPLICATION NUMBER: US/10/311,840
 ; CURRENT FILING DATE: 2003-12-18
 ; PRIORITY NUMBER: PCT/JP01/05263
 ; PRIORITY PILING DATE: 2001-06-20
 ; PRIORITY APPLICATION NUMBER: JP 2000-191088
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 1
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-311-840-1

Query Match 99.9%; Score 2276; DB 12; Length 525;
 Best Local Similarity 99.8%; Pred. No. 4.5e-173;
 Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 60
 Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 155
 Qy 61 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 120
 Db 156 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 215
 Qy 121 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 180
 Db 216 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 275
 Qy 181 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 240
 Db 276 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 335
 Qy 241 EGSNDIMGSTNFKELPGREGNRVDAAGTQPSKKEKRKEGSSDAESTN 300
 Db 336 EGSNDIMGSTNFKELPGREGNRVDAAGTQPSKKEKRKEGSSDAESTN 395
 Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 60
 Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNGKFEDGDDAISKLHDQBEYGAALIRNNQHIM 155
 Qy 61 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 120
 Db 156 GPVTAIKLGEENKENTPRVNLTIPASNYAKAHSKDKKKPQDQSKPVSKSTHR 215
 Qy 121 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 180
 Db 216 IQHNDYLKHLSKVKKIPSDFEGSCTDLOERGNDISPGDGOPFKD1PGKGATGPD 275
 Qy 181 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 240
 Db 276 LEGKDIQTFGPSPSAESTHLDTKPGTNEIPEREENGNTIGTRDETAKEADAVDVLV 335
 Qy 301 YNEIPKNGKGSTRGYDHSNRNQATLNKEQKRPFSKCKSQGLPISRGDNEIKNEMDSFN 360
 Db 396 YNEIPKNGKGSTRGYDHSNRNQATLNKEQKRPFSKCKSQGLPISRGDNEIKNEMDSFN 455
 Qy 361 GPSHENITTHGRKYHYVPHRQNNSTRANKGMPQGKGSWGRPHSNRFSRRDDSSBSSD 420
 Db 456 GPSHENITTHGRKYHYVPHRQNNSTRANKGMPQGKGSWGRPHSNRFSRRDDSSBSSD 515
 Qy 421 SGSSSESDGD 430
 Db 516 SGSSSESDGD 525

RESULT 4
 US-09-794-422-46
 ; Sequence 46, Application US/097944422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445
 ; CURRENT APPLICATION NUMBER: US/09/794,422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIORITY FILING DATE: 2000-09-22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 46
 ; LENGTH: 540
 ; TYPE: PPT
 ; ORGANISM: Homo sapiens
 ; US-09-794-422-46

Query Match 99.9%; Score 2276; DB 12; Length 540;
 Best Local Similarity 99.8%; Pred. No. 4.7e-173;
 Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNGFEDDDAISKLHDQEYGA
 Db 111 LNKEYSISNKENTHGLRMSIYKSTGNGFEDDDAISKLHDQEYGA
 Qy 61 GPVTAIKLGEENKENTPRVNNTIPASMYAKHSKDKKKP
 Db 171 GPVTAIKLGEENKENTPRVNNTIPASMYAKHSKDKKKP
 Qy 121 JOHNIDYKLHLSKVKKIPSDFEGSGYD
 Db 231 JOHNIDYKLHLSKVKKIPSDFEGSGYD
 Qy 181 LEGKDIDTGFA
 Db 291 LEGKDIDTGFA
 Qy 241 YNEIPKNGKGS
 Db 351 EGSDNDIMG
 Qy 301 YNEIPKNGKGS
 Db 427 YNEIPKNGKGS
 Qy 361 GPSHENILTHGRKYH
 Db 447 EGSDNDIMG
 Qy 401 YNEIPKNGKGS
 Db 461 EGSDNDIMG
 Qy 481 YNEIPKNGKGS
 Db 521 EGSDNDIMG
 Qy 541 YNEIPKNGKGS
 Db 591 EGSDNDIMG
 Qy 601 YNEIPKNGKGS
 Db 661 EGSDNDIMG
 Qy 681 YNEIPKNGKGS
 Db 721 EGSDNDIMG
 Qy 741 GPSHENILTHGRKYH
 Db 781 EGSDNDIMG
 Qy 801 YNEIPKNGKGS
 Db 841 YNEIPKNGKGS
 Qy 861 GPSHENILTHGRKYH
 Db 901 GPSHENILTHGRKYH
 Qy 921 SSSSES
 Db 951 SSSSES

RESULT 5
 US-09-794-422-46
 ; Sequence 8, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445

Query Match 99.9%; Score 2276; DB 12; Length 556;
 Best Local Similarity 99.8%; Pred. No. 4.7e-173;
 Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNGFEDDDAISKLHDQEYGA
 Db 127 LNKEYSISNKENTHGLRMSIYPKSTGNGFEDDDAISKLHDQEYGA
 Qy 61 GPVTAIKLGEENKENTPRVNNTIPASMYAKHSKDKKKP
 Db 187 GPVTAIKLGEENKENTPRVNNTIPASMYAKHSKDKKKP
 Qy 121 JOHNIDYKLHLSKVKKIPSDFEGSGYD
 Db 247 JOHNIDYKLHLSKVKKIPSDFEGSGYD
 Qy 181 LEGKDIDTGFA
 Db 307 LEGKDIDTGFA
 Qy 241 EGSDNDIMG
 Db 367 EGSDNDIMG
 Qy 301 YNEIPKNGKGS
 Db 427 YNEIPKNGKGS
 Qy 361 GPSHENILTHGRKYH
 Db 447 EGSDNDIMG
 Qy 401 YNEIPKNGKGS
 Db 487 GPSHENILTHGRKYH
 Qy 481 YNEIPKNGKGS
 Db 521 EGSDNDIMG
 Qy 541 YNEIPKNGKGS
 Db 591 EGSDNDIMG
 Qy 601 YNEIPKNGKGS
 Db 661 EGSDNDIMG
 Qy 681 YNEIPKNGKGS
 Db 721 EGSDNDIMG
 Qy 741 GPSHENILTHGRKYH
 Db 781 EGSDNDIMG
 Qy 801 YNEIPKNGKGS
 Db 841 YNEIPKNGKGS
 Qy 861 GPSHENILTHGRKYH
 Db 901 GPSHENILTHGRKYH
 Qy 921 SSSSES
 Db 951 SSSSES

RESULT 6
 US-09-794-422-46
 ; Sequence 2, Application US/09814550
 ; Publication No. US20020102641A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiavi, Susan
 ; APPLICANT: Madden, Stephen
 ; APPLICANT: Manavalan, Parthasarathy
 ; APPLICANT: Levine, Michael
 ; APPLICANT: Jan de Beur, Suzanne
 ; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
 ; FILE REFERENCE: 5014US

Query Match 99.9%; Score 2276; DB 12; Length 556;
 Best Local Similarity 99.8%; Pred. No. 4.7e-173;
 Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNGFEDDDAISKLHDQEYGA
 Db 127 LNKEYSISNKENTHGLRMSIYPKSTGNGFEDDDAISKLHDQEYGA
 Qy 61 GPVTAIKLGEENKENTPRVNNTIPASMYAKHSKDKKKP
 Db 187 GPVTAIKLGEENKENTPRVNNTIPASMYAKHSKDKKKP
 Qy 121 JOHNIDYKLHLSKVKKIPSDFEGSGYD
 Db 247 JOHNIDYKLHLSKVKKIPSDFEGSGYD
 Qy 181 LEGKDIDTGFA
 Db 307 LEGKDIDTGFA
 Qy 241 EGSDNDIMG
 Db 367 EGSDNDIMG
 Qy 301 YNEIPKNGKGS
 Db 427 YNEIPKNGKGS
 Qy 361 GPSHENILTHGRKYH
 Db 447 EGSDNDIMG
 Qy 401 YNEIPKNGKGS
 Db 487 GPSHENILTHGRKYH
 Qy 481 YNEIPKNGKGS
 Db 521 EGSDNDIMG
 Qy 541 YNEIPKNGKGS
 Db 591 EGSDNDIMG
 Qy 601 YNEIPKNGKGS
 Db 661 EGSDNDIMG
 Qy 681 YNEIPKNGKGS
 Db 721 EGSDNDIMG
 Qy 741 GPSHENILTHGRKYH
 Db 781 EGSDNDIMG
 Qy 801 YNEIPKNGKGS
 Db 841 YNEIPKNGKGS
 Qy 861 GPSHENILTHGRKYH
 Db 901 GPSHENILTHGRKYH
 Qy 921 SSSSES
 Db 951 SSSSES

RESULT 7
 US-09-794-422-46
 ; Sequence 2, Application US/09814550
 ; Publication No. US20020102641A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445

TYPE: PRT ; ORGANISM: Homo sapiens US-09-114-550-2

Query Match 99.6%; Score 2269; DB 10; Length 525; Best Local Similarity 99.5%; Pred. No. 1.6e-172; Mismatches 1; Indels 0; Gaps 0;

Matches 428; Conservative 1; Mi

Qy 1 VNKEYSIKENTINGLMSIYPSKSTGNKGFDGDDAISKLHQBEYGAALIRNMQHIM 60

Db 96 LNKEYSIKENTINGLMSIYPSKSTGNKGFDGDDAISKLHQBEYGAALIRNMQHIM 155

Qy 61 GPVTAIKLIGEENKENTPNVNLNIPASMYAKAHSKDKKKPORDSQAQKSPVKS- 120

Db 156 GPVTAIKLIGEENKENTPNVNLNIPASMYAKAHSKDKKKPORDSQAQKSPVKS- 215

Qy 121 IQRNDYLGHLSKVTKIPSDFEGSGYTDLQERGNDISPSGDCQPFKIDIPGKEATGPD 180

Db 216 IQRNDYLGHLSKVTKIPSDFEGSGYTDLQERGNDISPSGDCQPFKIDIPGKEATGPD 275

Qy 181 LEGKDIQTFAGPSEAFESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVDLY 240

Db 276 LEGKDIQTFAGPSEAFESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVDLY 335

Qy 241 EGNDIMGTSNFKELPGRGNRVDAGSONAHQGVFEPHPPASKEKEGSSDAESTN 300

Db 336 EGNDIMGTSNFKELPGRGNRVDAGSONAHQGVFEPHPPASKEKEGSSDAESTN 395

Qy 301 YNEIPKNGKGSTRKGVDHNRNQATLNEKORFSPKGKSCQGLPISRGLINEIKNEMDSFN 360

Db 396 YNEIPKNGKGSTRKGVDHNRNQATLNEKORFSPKGKSCQGLPISRGLINEIKNEMDSFN 455

Qy 361 GPSHENITTHGRKTHYVPRQNNSTRKGMPQKGWSGRQPHSNRFFSRDDSSSD 420

Db 456 GPSHENITTHGRKTHYVPRQNNSTRKGMPQKGWSGRQPHSNRFFSRDDSSSD 515

Qy 421 SGSSSESDGD 430

Db 516 SGSSSESDGD 525

RESULT 7 US-09-794-422-4

Sequence 4, Application US/09794422

PUBLICATION NO. US20030166239A1

GENERAL INFORMATION:

APPLICANT: Brown, Thomas A.

DE WET, Jeffrey R.

APPLICANT: Gowen, Lori C.

APPLICANT: Hanes, Lynn M.

APPLICANT: Hanes, Lynn M.

FILE REFERENCE: PC10445

CURRENT APPLICATION NUMBER: US/09794,422

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: 60/185,617

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 60/234,500

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4 LENGTH: 441

TYPE: PRT

ORGANISM: Mus musculus

US-09-794-422-4

Query Match 93.2%; Score 983.5; DB 12; Length 441; Best Local Similarity 50.5%; Pred. No. 3.6e-70; Mismatches 52; Indels 134; Gaps 8;

Matches 217; Conservative 52; Mi

Qy 6 SISNKENTINGLMSIYPSKSTGNKGFDGDDAISKLHQBEYGAALIRNMQHIMGPUTA 65

Db 34 SGRQDSTIKDLSAVVPPDVTDEGTEQDQGALLHPPGQDRYGAALIRNMQHIMGPUTA 93

Qy 66 IKLIGEENKENTPNVNLNIPASMYAKAHSKDKKKPORDSQAQKSPVKS- 122

Db 94 AELRREGNQEKRPQSVLSPVSIADYVNLKQTKNQESYLITQSSPVKSQHTKHTRQFTR 153

Qy 123 HNDYDYLGHLSKVTKIPSDFEGSGYTDLQERGNDISPSGDCQPFKIDIPGKEA- TGPPD 181

Db 154 RSTHYLTHLPOIJKTPSDLEGSSPDLLVQGDQHFMHIPGKGAGSGP- 212

Qy 182 EGKDIQTFAGPSEAFESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVDLY 241

Db 213 --SSTRPLGSSA2EVDPHMSGLGSNEIPGREGGGSAYATRDKAAGAGSAGSGLV 270

Qy 242 GSDNDIMGTSNFKELPGRGNRVDAGSONAHQGVFEPHPPASKEKEGSSDAESTN 301

Db 271 GSNEITGTSNFKELPGRGNRVDAGSONAHQGVFEPHPPASKEKEGSSDAESTN 329

Qy 302 NEIPKNGKGSTRKGVDHNRNQATLNEKORFSPKGKSCQGLPISRGLINEIKNEMDSFN 361

Db 330 NEIPKSSKGSSSDAEESKGNQNLTLTASQRFPKGKSGQPALSHLSNEVKSE- 383

Qy 362 PSHENITTHGRKTHYVPRQNNSTRKGMPQKGWSGRQPHSNRFFSRDDSSSD 420

Db 384 --EN-- HYVFGQNNLTPNKGMSQRGGSWPSRPNSHRASTRQR-DSSESSS 431

Db 421 SGSSSESDGD 430

Db 432 SGSSSESDGD 441

RESULT 8 US-09-794-422-2

Sequence 2, Application US/09794422

PUBLICATION NO. US20030166239A1

GENERAL INFORMATION:

APPLICANT: Brown, Thomas A.

DE WET, Jeffrey R.

APPLICANT: Gowen, Lori C.

APPLICANT: Hanes, Lynn M.

FILE OF INVENTION: Mammalian Osteoregulins

FILE REFERENCE: PC10445

CURRENT APPLICATION NUMBER: US/09794,422

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: 60/185,617

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 60/234,500

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 435

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-794-422-2

Query Match 41.2%; Score 938.5; DB 12; Length 435; Best Local Similarity 49.4%; Mismatches 45; Indels 146; Gaps 8;

Matches 211; Conservative 45;

Qy 9 NKENTHNGLMSIYPSKSTGNKGFDGDDAISKLHQBEYGAALIRNMQHIMGPUTA 128

Db 29 NQENTH--LASTKPEPKVKGTEGRDAPLFLDQNRRQATLRLNTQPVSLVGTTEV 85

Qy 69 LGHENKENTPNVNLNIPASMYAKAHSKDKKKPORDSQAQKSPVKSQHTKHTRQFTR 145

Db 86 QSDRNKEKIPSDFEGSGYTDLQERGNDISPSGDCQPFKIDIPGKEA- --GKD 145

Qy 129 KHLISKVTKIPSDFEGSGYTDLQERGNDISPSGDCQPFKIDIPGKEA- --GKD 185

Db 146 THPQKILSDFASPDLLVQGDQHFMHIPGKGAGSGP- 205

Qy 186 IGTGEAGPSEAFESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVDLY 245

Db 206 V---SGSSNVEIVDPHTNGLGSNETPGREHHIGGAYATRGKTAQGAGSSADVSLVFGSNE 261
 Qy 246 IMGSTNPKELPGREGNRVDAAGSONAIIQGKVFHYPPAKPSKERKKEGSSDAAESTNNEIP 305
 Db 262 ITGSTKPERLPKSEGKRVDAQNSQNAHGKVEPHQPSKERKVGSSREHKGAGYNEIP 321
 Qy 306 KNGKGSRKYDHSNRRNQATLINEKORFSPSKGSQGLPIPSRGKLDNEIKNEMDSFGNSH 365
 Db 322 KSSKGASKDAEESKGKRNQVLTIESQRPGKGRGQS---SHSLGNEVKSKEDSSNLSRE 377
 Qy 366 NI-IITGKRYHVVPHQRRNNSPENKGMFQGKSSW-GROPHSNRFSRRDDSESSDGS 423
 Db 378 GIAIAHRTSH-----PTTRNQGMSQRGSWASRPRPHRVRVSTRQR-DSSSESSSSGS 428
 Qy 424 SSESQGD 430
 Db 429 SSESQGD 435

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptidic compound
 US-09-812-485A-2

Query Match 10.0%; Score 246; DB 10; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 108 AQKSPVSKSKSTRHIONTIDYLKHLSSKVKK1PSDFEGSGYTDQERGD 154
 Db 1 AQKSPVSKSKSTRHIONTIDYLKHLSSKVKK1PSDFEGSGYTDQERGD 47

RESULT 9

US-09-812-485A-1
 ; Sequence 1, Application US/09812485A
 ; Publication No. US20020197267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari
 ; APPLICANT: Blacher, Russell
 ; APPLICANT: Yoneda, Toshiyuki

; TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 97
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptidic compound
 US-09-812-485A-1

Query Match 10.0%; Score 246; DB 10; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 108 AQKSPVSKSKSTRHIONTIDYLKHLSSKVKK1PSDFEGSGYTDQERGD 154
 Db 1 AQKSPVSKSKSTRHIONTIDYLKHLSSKVKK1PSDFEGSGYTDQERGD 47

RESULT 12

US-09-812-485A-3
 ; Sequence 3, Application US/09812485A
 ; Publication No. US20020197267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari
 ; APPLICANT: Blacher, Russell
 ; APPLICANT: Yoneda, Toshiyuki

; TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

RESULT 10

US-09-812-485A-2
 ; Sequence 2, Application US/09812485A
 ; Publication No. US20020197267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari
 ; APPLICANT: Blacher, Russell
 ; APPLICANT: Yoneda, Toshiyuki

; TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: peptidic compound
 US-09-812-485A-3

Query Match Similarity 10.0%; Score 229; DB 10; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 AQKSPVRSKSTRIQHNIDYLKHLISKVKKIKPSDFEGSGYTDLQE 151
 Db 4 AQKSPVRSKSTRIQHNIDYLKHLISKVKKIKPSDFEGSGYTDLQE 47

RESULT 13
 US-09-812-485A-23

Sequence 23, Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:
 APPLICANT: Blacher, Russell
 ATTORNEY: Yoneeda, Toshiyuki

APPLICANT: Kumagai, Yoshinari
 ATTORNEY: Blacher, Russell

APPLICANT: Yoneeda, Toshiyuki
 ATTORNEY: Peptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: US/09/641,034
 FILE REFERENCE: BEAR-006CIP

NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 23
 LENGTH: 0

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptidic compound

US-09-812-485A-23

Query Match Similarity 100.0%; Score 218; DB 10; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 RGDNIDSPFSGDQGPFFKIDPGKGEATGPDLGKDIQGFA 191
 Db 1 RGDNIDSPFSGDQGPFFKIDPGKGEATGPDLGKDIQGFA 40

RESULT 14
 US-09-812-485A-6

Sequence 6, Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 ATTORNEY: Blacher, Russell

APPLICANT: Yoneeda, Toshiyuki
 ATTORNEY: Peptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: US/09/641,034
 FILE REFERENCE: BEAR-006CIP

NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 4

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptidic compound

US-09-812-485A-6

Query Match Similarity 88.0%; Pred. No. 2.4e-10;
 Matches 44; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 105 DSQAQKSPVRSKSTRIQHNIDYLKHLISKVKKIKPSDFEGSGYTDLQE 154
 Db 1 DSQAQKSPVRSKSTRIQHNIDYLKHLISKVKKIKPSDFEGSG-----RGD 44

RESULT 15
 US-09-812-485A-5

Sequence 5, Application US/09812485A
 Publication No. US20020197267A1

GENERAL INFORMATION:
 APPLICANT: Kumagai, Yoshinari
 ATTORNEY: Blacher, Russell

APPLICANT: Yoneeda, Toshiyuki
 ATTORNEY: Peptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases

CURRENT APPLICATION NUMBER: US/09/812,485A
 CURRENT FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: US/09/641,034
 PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5

LENGTH: 44

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptidic compound

US-09-812-485A-5

Query Match Similarity 9.4%; Score 215; DB 10; Length 44;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 SPVKSKSTRIQHNIDYLKHLISKVKKIKPSDFEGSGYTDLQE 151
 Db 4 SPVKSKSTRIQHNIDYLKHLISKVKKIKPSDFEGSGYTDLQE 44

Search completed: November 26, 2003, 15:53:39
 Job time : 38 secs

13	137	5	PCT-US94-04496-25	Sequence 25, App1
14	134.5	5.9	9391 4084 2	Sequence 1, App1
15	134.5	5.9	US-08-168-459A-1	Sequence 1, App1
16	134.5	5.9	US-08-167-566B-1	Sequence 1, App1
17	134.5	5.9	US-09-210-288-1	Sequence 1, App1
18	129	5.7	5198347-5	Patent No. 5198347
19	127.5	5.6	5198347-3	Patent No. 5198347
20	127	5.6	3707 1	Sequence 1, App1
21	127	5.6	US-08-118-101A-1	Sequence 1, App1
22	126.5	5.6	2695 4	Sequence 3, App1
23	126.5	5.6	US-09-170-242-1	Sequence 295, App1
24	125.5	5.5	4215 4	Sequence 12, App1
25	125.5	5.5	1393 5	Sequence 1, App1
26	124.5	5.5	3773 3	Sequence 1, App1
27	123	5.4	3825 3	Sequence 2, App1
28	123	5.4	US-09-130-242-3	Sequence 2, App1
29	123	5.4	3552 4	Sequence 3, App1
30	123	5.4	US-09-130-242-3	Sequence 3, App1
31	122.5	5.4	5173 4	Sequence 2, App1
32	122.5	5.4	3552 4	Sequence 2, App1
33	122	5.4	1503 3	Sequence 693, App1
34	122	5.4	3534 4	Sequence 11, App1
35	121	5.3	4766 5	Sequence 2269, App1
36	121	5.3	6775 4	Sequence 10, App1
37	121	5.3	3347 4	Sequence 289, App1
38	121	5.3	3347 4	Sequence 318, App1
39	121	5.3	2073 4	Sequence 318, App1
40	121	5.3	43280 2	Sequence 1731, App1
41	121	5.3	2004 1	Sequence 1, App1
42	121	5.3	2004 1	Sequence 1, App1
43	121	5.3	2004 2	Sequence 18, App1
44	121	5.3	2004 2	Sequence 18, App1
45	121	5.3	2655 2	Sequence 17, App1

סודות גראן צ'רץ

RESULT 1
US-08-931-999-4
Sequence 4, Application US/08931199
; Patent No. 6043219
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; APPLICANT: Crupper, Scott S.
; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City

SUMMARIES						
Suit No.	Score	Query	Match	Length	DB	ID
1	150	6.6	6755	3	US-08-531-999-4	Sequence 4, Appli
2	140	6.1	6929	1	US-08-541-751-11	Sequence 11, Appli
3	138.5	6.1	2384	1	US-07-814-964-10	Sequence 10, Appli
4	138.5	6.1	2384	1	US-08-258-442-10	Sequence 10, Appli
5	138.5	6.1	2384	1	US-08-328-803-10	Sequence 5, Appli
6	138.5	6.1	2384	4	US-08-866-840-5	Sequence 5, Appli
7	138.5	6.1	2384	5	PCM-US92-11107-10	Sequence 10, Appli
8	137	6.0	9370	1	US-08-340-559-27	Sequence 27, Appli
9	137	6.0	9370	3	US-08-545-860D-27	Sequence 27, Appli
10	137	6.0	9370	5	PCM-US94-04496-27	Sequence 27, Appli
11	137	6.0	9391	1	US-08-250-559-25	Sequence 25, Appli
12	137	6.0	9391	3	US-08-345-860D-25	Sequence 25, Appli

SUMMARIES		Description			
Result	No.	Score	Query Match	Length	ID
1	150	6.6	6755	3	US-08-931-999-4
2	140	6.1	2690	1	US-08-524-057-11
3	138.5	6.1	2384	1	US-07-814-964-10
4	138.5	6.1	2384	1	US-08-258-442-10
5	138.5	6.1	2384	1	US-08-328-809-5
6	138.5	6.1	2384	4	US-08-866-840-5
7	138.5	6.1	2384	5	PCT-US92-11107-10
8	137	6.0	9370	1	US-08-320-559-27
9	137	6.0	9370	3	US-08-545-860D-27
10	137	6.0	9370	5	PCT-US94-04496-27
11	137	6.0	9391	1	US-08-320-559-25
12	137	6.0	9391	3	US-08-545-860D-25

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25043-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057

SEQUENCE CHARACTERISTICS:
 LENGTH: 6755 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Staphylococcus aureus*
 STRAIN: UT0007
 US-08-911-999-4

Alignment Scores:
 Pred. No.: 0.000155 Length: 6755
 score: 150.00 Matches: 104
 Percent Similarity: 31.05% Conservative: 59
 Best Local Similarity: 19.81% Mismatches: 201
 Query Match: 6.58% Indexes: 162
 DB: 3 US-09-700-696c-2 (1-430) × US-08-931-999-4 (1-6755)

QY 2 AsnLySGLutYrSerLsSerAsnLysGluAsnThrHisAsnGlyLeuLrgMetSerIle 21
 DB 4164 AACCCAAAACAAAGCAAGGAAAGCCACCCACAAACGACAGGCAA----- 4217

QY 22 TyrProLysSerThrGlyAsnLysGluAspGlyAspAspAlaLysSerIle 41
 DB 4218 ---AGGAAAACGGGGAAA-----AAGGACCCAAAAAAACAAACAAACA 4259

QY 42 HisAspGlnGlu-----45
 DB 4260 CACAGAGGAAACGGGACACAAACAGCGGAGAAACCCAGAAACAAACAAA 4319

QY 46 ---GluTyrclyAlaAlaLysIleArgAsnAsnMetGlnIleMetGlyProValThr 64
 DB 4320 GGAAAAAAACCGAAAACACAAACGAAACAAAGAAAGGAAAGCCGAAAA 4379

QY 65 AsnLysLysIleLeuGlyGluGluLysIleGlyAsnValLeuAsnIle 84
 DB 4380 AGAACAAA-----AAAACAAAACACAAACGAGAACCCCACAAACAAAACA 4433

QY 85 IleProAlaSerMetAsnTyrrAlaHisSerLysIleAspLysLysIspGlnArg 104
 DB 4434 CAAGGACGAGAAACGGGAAACCCAGAAACGAGAAACAAAGGAAACAAAAG 4493

QY 105 AspSerGlnAlaGin-----Lys 110
 DB 4494 GAAAGAAANACCAACCAAGCAGAAAGGCAAAACGAAACAAACAAAAGAA 4553

QY 111 SerProValLys-----SerIleSerThrHisArgIleGlnHiAsn 124
 DB 4554 ACACCCGAAAAAACAAACAAACCAACCCAAAGGAAAGAGAAGAGAAC 4613

QY 125 IleAspTyrclyIleLysIleSerLysValLysIleProSerAspPheGluGlySer 144
 DB 4614 -----ACAACGAAAAA-----GAAACCGGGAGGGAGA 4643

QY 145 GlyTyrrAspLeuGlnGluIrgLysGlyAspAspIleSerProPheGlyAspGly 164
 DB 4644 GGAAACAGCCAGAAAACAGACAACCAACGAAACGGGGACAGAAACAAAAGGC 4703

QY 165 GlnProPhelysAspIleProGlyLysGlyGluAlaIrgLysProAspIleGluGlyLys 184
 DB 4704 -----AAAACGAGAGGCAAAACGAAACGAAACAGAACACAAAGAAA 4754

QY 185 AspIleGln-----187
 DB 4755 GAAAACAGAAACGGAAACGAAACAGAGAAACAAACGACAAAGCAACAAA 4814

QY 188 -----ThrclypheAlaLysGlyProSerGluAlaIleSerThrHis 200
 DB 4815 AAAAGGGCCGACGGACACAAAAAGGAAAGAGACACCCCCAC 4873

Db 201 LeuAspThrLysLys-----205
 Qy 4874 ACCGAGAAAACAAAGACAACGAAACGAAACGAAACGGGC 4933

Db 206 -----ProGlyTyrsAsnGluIleProGluIrgArgGlu 215
 Qy 4934 AAAAGAGGAAAACGAAAAGAAAGAAAGACAGAAAAGGAGAGAAAAC 4993

Db 216 GluAsnGlyLysAsnThrIleGlyThrAspGluThrAlaLysGluAlaAspAlaVal 235
 Qy 4994 CACAGCCGGGCCCCAACGAAAGCAGCACGAAACGGGAA-----5083

Db 236 AspValSerIeuvAluGluGlySerAsnAspIleMetGlySerThrAsnPhelysGluLeu 255
 Qy 5045 -----AAACAAAAACACCAAAAGGCAAAACCCAAAGGACCA 5083

Db 256 ProGlyArgelysGluAsnArgValAspAlaLysGlySerGlnAsnAlaIahisGlnGlyLysVal 275
 Qy 5084 AAAACAGGGCGAGG-----CAAGCGGC-----5128

Qy 276 GluPheHistYrProProAlaProSerLysGluIrgLysGluGlySerSerAspAla 295
 DB 5129 AGAGGGAAACACAAAACCGGAAACGGGACAAAGGGAAAGGGAAA-----5182

Qy 296 AlaGluSerThrAsnTyrrAsnGluIleProLysGlnGlySerThrArgLysGly 315
 DB 5183 -----AAAGAGAAAAGGGACAGGGGAGGGCAAGAGGAACGGCCAAACG 5224

Qy 316 ValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluIlyGlySerGlnArgSerProSerLys 335
 DB 5225 AAAAGAGAAAACGGGACCCAGAAACGAAACACGAAACGAAACGAAACG 5284

Qy 336 -----GlyLysSerGlnGlyLeuProSerArgGlyLeuAspAsnGluIleLys 353
 DB 5285 AAAACGGGAAAAGCA-----5302

Qy 354 AsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLys 373
 DB 5303 ---AAAAGAACACAAACGAGGACAGAACGAAACGAAAC-----5350

Qy 374 TyrHistYrValProHisIleArg-----GlnAsnAspSerThr 385
 DB 5351 AGAGGGAAAACCAACACCCGAAACGAAAGGACAAGCAACGAAACGAAACG 5410

Qy 386 ArgAsnLysGlyMetProGlnGlySerIrrpGlyArgGlnProHisSerAsnArg 405
 DB 5411 AGAAAGGGAAANGAAAMAAAGAAAMAAAGAAACAAACGCGGAAGGCCAGGA 5470

Qy 406 ArgPheSerSerSerArgArgAspSerSerGluUserSerAsp-----SerglySerSer 424
 DB 5471 AGAAAGGGAAAGCCAAAGGAGAAAGGAGAAACGAGAAACGAGAAAGGGAA 5530

Db 5425 SerGluUserAspGly 429
 DB 5531 ACCCACAAAGCGGA 5545

RESULT 2

US-08-524-757-11

Sequence 11, Application US/08524757

; Patent No. 5792634

; GENERAL INFORMATION:

; APPLICANT: Conway, Ronald C.

; ATTORNEY: Bradsher, John N.

; TITLE OF INVENTION: RNA Polymerase Transcription Factor

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS

; STREET: 1201 Elm Street, Suite 4500

; CITY: Dallas

; STATE: TX

COUNTRY: US
 ZIP: 75270-2197
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 COMPUTER: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/524,757
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/13621
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/160087
 FILING DATE: 30-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Harre, John A.
 REGISTRATION NUMBER: 37,345
 REFERENCE/DOCKET NUMBER: B35006C1PC1P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (214) 939-4500
 TELEFAX: (214) 939-4600
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2690 base pairs
 TYPE: nucleic acid
 STRANDBNESS: both
 TOPOLOGY: both
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 33...2351
 US-08-524-757-11

Alignment Scores:
 Pred. No.: 0.00039
 Score: 140.00
 Percent. Similarity: 32.08%
 Best Local Similarity: 20.52%
 Query Match: 6.14%
 DB: 17

US-09-700-696C-2 (1-430) x US-08-524-757-11 (1-2690)

Qy 23 ProLysserThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerlysLeuIle 42
 Db 660 CCTCGGAAAGGCCACGCCATGCCATGCCCTTCAGGACAGACTGGGCAAGAACGACAC 719

Qy 43 AspGlnGluGluLysTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyPro 62
 Db 720 CCGGTTGAACTCCATGGAAAGGGTGTGAGTCAAACCAAGGAGCAC--- 767

Qy 63 ValThrAlaIleLysLeuIleGlyGluGluAsnLysGluAsnThrProArgAsnValLeu 82
 Db 768 -----AAATCTTCACAGGCAAAAGCCCCGTG 797

Qy 103 GlnArgAspSerGlnAlaGlnLysSerThrIleSerlysSerProValLysSerlysLeuIle 122
 Db 798 GATGCCAAGATGATGAGAAAGGCCCTGTGTTGAGCAGAGAAATCACAC 848

Qy 123 HisAsnIleAspTyrLeuIshisIleSerlysVallysLysIleProSerAspPheGlu 142
 Db 849 -----AAGGCCCTTCACAA----- 863

Qy 143 GlySerGlyTyrThrAspLeuGluArgGlyAspAsnAspIleSerProheSerGly 162
 Db 864 -----GAGGAAACGAAAGCCACCCCTAGGG 890

Qy 163 AspGlyGlnProhePheLysPheProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
 Db 891 GACATGCAAGGGAAACCG---CCCTCTAGTGTGGCTTAAAGAAGAGGACAGAGAG 947

Qy 183 GlyLysAspIleGlnIleSerlysLysIleProSerGluAlaGlyProAspSerGluIle 201
 Db 948 GGCGAGGCTTGAGAAGAGACTGTTGCCCTCAGAGGCCGCTTACAGAACACCTG 1007

Qy 202 AspThrLysAspProGluArgGluGluAsnGlyGlyAsnThr 221
 Db 1008 -----AAAAGCCAAGCAAGGAC---CCAGAAAGGCCAA----- 1043

Qy 222 IleGlyThrArgAspPgluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
 Db 1044 -----TTGGACAAAGCAAGGAAAGCTCTGGACAGCTTGACACAGGA-----AAA 1088

Qy 242 GlySerAspAspIleMet-----GlySerThrIshisPheLysGluLeu 255
 Db 1089 GGAGGAGGAGACCTGTCGCCAAAGGTTCTAACACCTAAAGACTCCA 1148

Qy 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyysVal 275
 Db 1149 GAAAGGAAGGTCAAAACTATTGATGATAAAAGTCATCTGGCTC---CTCCCTAAAGT 1205

Qy 276 -----GluPheHisTyrPro----- 280

Db 1206 GAGGAGACAGATAGGAGATGATTGAGCCACCATGTCCTTGTATCCACCTRC 1265

Qy 281 -----ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSer 298
 Db 1266 AGCTATGACCGAGCCGGAGAAAAGAAAAGATTGTGAAACT---TCAGCCACGGCA 1322

Qy 299 ThreonineAsnGluIleProLysAsnGlySerThrArgLysGlyValAspHis 318
 Db 1323 CTTGAGATAAAAGACTTAAAAGAAATTGACTCTAAAGGACTGTGTAAAACTTGATCACTCA 1382

Qy 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyTyrSer 338
 Db 1383 GTTAAAGAAATTACCCAAAGTGACAAAAACAAAGTCAGAGAAAGCCGTTGAGCTGATTTA 1442

Qy 339 GlnglyLeu----- 341
 Db 1443 GCCAAAGCTGAGAAAGGTGCCTGATGTTGCCAGTGTGCCAGACCTCCCGTACCCGGG 1502

Qy 342 -----ProIleProSerArgGlyLeuAspAsnGlyLysIleSerGlu 355
 Db 1503 ATACAGGCCAATTAACGCCACAGCCCTTCCTCGAGCTGATATCCTCTTCAGGCCAAG 1562

Qy 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
 Db 1563 CGAAAGGCTCTCCAGGAAAGAGCTGATTCTGGGAGAATG 1622

Qy 367 -----IleIleThrHisGlyArgLysTyrIleIleValPro----- 378
 Db 1623 AATCCCAAGATGGCTTATCTGGTCAACTGTGCTATCTCCCTAAATGATGAC 1682

RESULT 3
 US-07-814-964-10
 ; Sequence 10, Application US/07814964
 ; Patent No. 5,353047
 ; GENERAL INFORMATION:
 ; APPLICANT: Donahue, Brian A.
 ; APPLICANT: Toney, Jeffrey H.
 ; APPLICANT: Brahn, Suzanne L.
 ; APPLICANT: Pil, Pierer M.
 ; APPLICANT: Brown, Steven
 ; APPLICANT: Kellett, Patti
 ; APPLICANT: Essigmann, John M.

APPLICANT: Lippard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/814,964
 FILING DATE: 19911226
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-4787AAA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2384 base pairs
 CLONE: Drosophila SSRP - composite sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 2
 MAP POSITION: 60A 1-4
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 123 .. 2291
 US-07-814-964-10

Alignment Scores:
 Pred. No.: 0 0.000459 Length: 2384
 Score: 138.50 Matches: 99
 Percent Similarity: 31.91% Conservative: 50
 Best Local Similarity: 21.90% Mismatches: 136
 Query Match: 6.08% Indels: 182
 DB: 1 Gaps: 23

US-09-700-696C-2 (1-430) x US-07-814-964-10 (1-2384)

Qy 16 GlyLeuIhrMetSerIleItyrProLyserThrGly-AspLySGlyP
 Db 1187 GGCGCAGGATTCATCATATCCAAAGCCACCGCTGATCCGCT
 Qy 35 pAspAlaIleSerIleLeuIhsApgIglGluGluItyrGlyAla---
 Db 1242 -----ATTAGTTCTGATGCTGCAAGTCAGCTGGCCAGCTCCACGC
 Qy 50 ---AlaLeuIleArgAsnAsnMetGlnIisIleMetGlyProVal
 Db 1295 CGAAAGTGCAGGCTAAAGACCGAAATGTTGATCTCTCCATC-
 Qy 68 uIeuGlyIglGluAsnIlySGluAsnThrProArgAsnValLeuAsnI

Qy 413 PAspSerGluSerAspSerGlySerSerGlu----- 426
 Db 2117 CGAGCACTCACCAGTCCACGAGAACAGAGAAAGGACAAAGGCTGCCAAGAGAAAGC 2176
 Qy 427 -----SerAspGlyAsp 430
 Db 2177 GCCCCATCGACCGCGAT 2195

RESULT 4
 / Sequence 10, Application US/08258442
 / GENERAL INFORMATION:
 / APPLICANT: Donahue, Brian A.
 / APPLICANT: Toney, Jeffrey H.
 / APPLICANT: Bruhn, Suzanne L.
 / APPLICANT: Pil, Peter M.
 / APPLICANT: Brown, Steven
 / APPLICANT: Kelleit, Patti M.
 / APPLICANT: Essmann, John M.
 / APPLICANT: Lippard, Stephen J.
 / TITLE OF INVENTION: DNA structure Specific Recognition
 / NUMBER OF SEQUENCES: 13
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 / STREET: 2 Militia Drive
 / CITY: Lexington
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02173
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: FLOPPY disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/258,442
 / FILING DATE:
 / CLASSIFICATION: 530
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/539,906
 / FILING DATE: 18-JUN-1990
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Granahan, Patricia
 / REGISTRATION NUMBER: 32,227
 / REFERENCE DOCKET NUMBER: MIT-4787AA
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 617-861-6240
 / TELEFAX: 617-861-9540
 / INFORMATION FOR SEQ ID NO: 10:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 2384 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / ORIGINAL SOURCE: Drosophila melanogaster
 / IMMEDIATE SOURCE:
 / CLONE: Drosophila SSRP - composite sequence
 / POSITION IN GENOME:
 / CHROMOSOME/SEGMENT: 2
 / MAP POSITION: 60A 1-4
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 123..2291
 / US-08-258-442-10
 / Alignment Scores:
 / Pred. No.: 99
 / Score: 304
 / Length: 2384
 / Matches: 99

Percent Similarity: 31.91%
 Best Local Similarity: 21.20%
 Query Match: 6.08%
 DB: 1
 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-258-442-10 (1-2384)

Qy 16 GlyLeuArgMetSerIleTyrProLysserSerThrGly-AsnLysGlyPheGluAspGlyAs 35
 Db 1187 GGAGCGAGCATCATATCCAAAGCACCCGATATCCCCTTGAGGAG----- 124
 Qy 35 pAspAlaSerLysLeuHisAspGlnGluGluGlyGlyAla----- 49
 Db 1242 -----ATTAGTCTGAACTTGGCCAGGGCGATCCAGGCATCTTGACTTGCATT 1299
 Qy 50 -----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLeuLysL 68
 Db 1295 CGAAGTGGCCCTAACGACGGAACTGTGAACTCTCTCTCCAC----- 134
 Qy 68 uLeuGlyGluGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleProAlaAs 88
 Db 1341 -----GAGAAGGAGG----- 135
 Qy 88 zMetAsnTyrAlaAlaHisSerIleAspLysLysProGlnArgAspSerGlnAl 108
 Db 1353 -----TATGCCAAGGTC----- 136
 Qy 108 aglnLysserProValLysSerIleSerThrHisArgleGlnHisAsnIleAspTyrle 128
 Db 1365 -----TTCGAATCAT 137
 Qy 128 uLys-----HisLeuSerLysValLysIleProSerAspPheGluGlySe 144
 Db 1376 CRACACAGAGAACTTGCAATGTCAGATGGCCAAAG-----GAAAGAG 142
 Qy 144 rGlyTyrThrAspLeuGlnGluArgGlyAspPanaAspIleSerProPheSerGlyAspG 164
 Db 1421 CGGCTCTAACGGCCTG-----GACTTTGGTGTACGGAC-----AACGAGAA 146
 Qy 164 yGlnProPheIysAspIleProGly-----LysGlyGluAlaThrGlyProAspLeuGluG 183
 Db 1463 CGAACAGATGCCCTAAGGTGAGCGCTAAGGTGAGCGAGGAAAGGAGGAGCGA 152
 Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluSerThrHisLeuAspTh 203
 Db 1523 CGACGAT-----GGCGACTCTGGATGAAGACTCAGGGATGAGGACTT 156
 Qy 203 rLysLysProGlyTyrLysGluIleProGluArgGluLysGluGlyAsnThrIleG 223
 Db 1565 C---AAGCCCCAACGAGAACGAGCTCCATGTGCCAGGATGAGCAG 162
 Qy 223 yThrArgAspGluThrAlaLysGluIleAspAlaValGluGlySe 243
 Db 1622 TGATTCGACAT-----GACGCGATCTGATGCG-----GGCG 165
 Qy 243 rAsnAspIleMetGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsnArgVa 263
 Db 1658 AGGCACAGCGACGGCCAGGGCAAGAAAAGAAGGAGAAAGTCGAGAAAGGAAAAA 171
 Qy 263 IAspAlaGlySerGlnAlaIaHisGlyLysValGluAspValSerLeuValGluGlySe 283
 Db 1718 GGAGAAGAAACACAGAGGAGGAAACAG-----ThAsnTyrrAsnGluII 304
 Qy 283 oSerIysGluIysArgLysGluIysSer-----AAACC 175
 Db 1757 CTCCAGAAAGAGAACGACTCTGGCAAAACCCAAAGGCCAACCCCTTCATGGCTCTG 181
 Qy 293 ---SerAspAlaAlaGluSer-----AAAC 175
 Db 1817 GCTGAAACGACAGCGGAGGACATCPAGGGAAAAATCGGGCATTAAGGTACCGAGAT 187
 Qy 304 eProlysAsnGlyIysGlySerThrArgLysGlySerAsnAspGlnAl 324

RESULT 7
PC-TUS92-11107-10
Sequence 10, Application PC/TUS9211107
GENERAL INFORMATION
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Brumley, Suzanne L.

Db	1187	GGAGCCAGGATTCATCTATAACCAAGGCCACCGCTGATATCGGTTGGAG---	1241
Qy	35	PASPAlaIleSerLysLeuHisAspGlnGluGluIutyrGlyAla-----	49
Db	1242	-----ATTAAGTCTGTCGAACTTGGCCGGCGGATCCACGGGATCTTCGACTT	1294
Qy	50	AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaLeuLysLe	68

APPLICATION NUMBER: US 08/062, 443
 FILING DATE: 14-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/971, 094
 FILING DATE: 30-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/888, 839
 FILING DATE: 27-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/805, 093
 FILING DATE: 11-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Esq., Mark
 REGISTRATION NUMBER: 33, 2229
 REFERENCE/DOCKET NUMBER: TJU-1262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9370 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 469..4032
 US-08-545-860D-27

Alignment Scores:
 Pred. No.: 0 00499
 Score: 137.00
 Percent. Similarity: 34.70%
 Best Local Similarity: 21.55%
 Query Match: 6.01%
 DB: 3

US-09-700-696C-2 (1-430) x US-08-545-860D-27 (1-9370)

Qy 37 AlaIleSerIlysLeuHisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnAsnMet 56
 Db 1938 GAGCTGACACTGGTACAAAGGCCAGCCAGCTGGCCACAGGGCCAG 1997

Qy 57 GlnHistIleMetGlyProValIthrAlaIleIlysLeuLeuGlyGluGluAsnIlysGluAsn 76
 Db 1998 GAGCAC---AGAGCCCCAACGGGACCCAGAGTAAGGCAAGCAGAGTCAC 2054

Qy 77 ThrProArgAsnValLeuAsn-----IleLeuProAlaSerMetAsnTyAlaIlysAla 94
 Db 2055 GAGTC-AGGGCATTCGAATCAAAGATCCTMCCCC-----CTAAAGCT 2098

Qy 95 HisSerIlysAspIlysLysProGlnIarg-----AspSerGlnAlaGln 109
 Db 2099 CC-AGCRAAGGCCGCCCCACCCGGAAAGGCCCAAGGGCTACGGAGCTGCA 2157

Qy 110 LysSerProAlaIlysSerThrHisArgIleGlnHisAsnIleAspTyrLeuIys 129
 Db 2158 AGTGTCCGGCACAGGGCACAGGAAAGCCCAAAACGTTGGAACGCCAAACCCAA 2217

Qy 130 HisLeuSerIlysValLeuAspSerIlysProSerAspPhedIuGlySerGlyTyrThrAspLeu 149
 Db 2218 -----DRAACCTGTCAGGGCCTRTGCCCGGGCGAGGAAGCAACCCAA 2262

Qy 150 GlnGluArgGlyAspAsnAspIleSerProHeSerGlyAspDglyIinProHeIysAsp 169
 Db 2263 CAGGGGAAAGGGAGGGCACGGCTTCTCCCTPATGGCTCCGAGCCAGACTTCAGAACAGAC 2322

Qy 170 IlePro-----GlyLysGlyIglu----- 175
 Db 2323 AAGGCCAAGGTCAAGGAAGGAGCCGGCCGGCCAGGAAGCAACGCCAAAGCC 2382

Qy 176 AlanArgIlysProAspIleGluGlyIgluIlysAspDleGlnThrGlyPheIgluProSerGly 195

RESULT 10
 PCT-US94-04496-27
 ; SEQUENCE 27, APPLICATION PC/TUS9404496
 ; GENERAL INFORMATION:
 ; APPLICANT: Croce, Carlo
 ; APPLICANT: Canaani, Eli
 ; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 ; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 ; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
 ; NUMBER OF SPECIMENS: 95

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
 ADDRESS: Norris
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLucia Esq., Mark
 REGISTRATION NUMBER: 33-229
 REFERENCE/DOCKET NUMBER: TJJU-1242
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9370 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 469 .. 4032
 PCT-US94-04496-27

Alignment Scores:
 Pred. No.: 0.00499
 Score: 137.00
 Percent Similarity: 34.70%
 Best Local Similarity: 21.55%
 Query Match: 6.01%
 DB: 5
 Length: 9370
 Matches: 100
 Conservative: 61
 Mismatches: 192
 Indels: 113
 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-27 (1-9370)

Qy 37 AlarileSerIlyLeuHisAspGlnGluItyrGlyAlaAlaLeu
 ||||| :
 Db 1938 GCAGCTGGACAACTGGCTGACCAAGTCAGCCAGCTGGCC
 ||||| :
 Qy 57 GlnHisIleMetGlyProValThrAlaLeuLeuGlyGlu
 ||||| :
 Db 1998 GAGCAC --AGAGCCCCACCGGACCCAGAGATAAGGGCAGGG
 ||||| :
 Qy 77 ThrProArgAsnValLeuAsn---IleLeuProAlaSerMetIle
 ||||| :
 Db 2055 GAGTC-AGGACATTCTGAATCAAAGATCCCTCCC--
 ||||| :
 Qy 95 HisSerLysAspLysLysProGlnArg--
 ||||| :
 Db 2099 CC-AGCAAAGCCCCGGCCACCGGAAGCCCCACCCGGAA
 ||||| :
 Qy 110 LysSerProValLysSerIleThrHisArgIleGlnHisAsnIle
 ||||| :
 Db 2158 AAGTCCTGGCAAGCGAGGCCCCACAAAGCAAACCGTGGAA
 ||||| :
 Qy 130 HisLeuSerIlyValLeuLysIleProSerIspPheGluGlySer
 ||||| :
 Db 2218 -----AAACCTGTCAGGGCCTTCCTCCATGCGCCGAGGTT
 ||||| :
 Qy 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGly
 ||||| :
 Db 2263 CAGGGGAAAGGGCAGGGCAGGCTTCCTCCATGCGCCGAGGTT
 ||||| :

QY	170	IlePro-----GlyLysGlyGlu-----	175
Db	2323	AAGCCCAGGTGAGAACGAAAGGCCGGCCGGACCAAGGAACCCAAAGCCA	2382
QY	176	AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPhAlaGlyProSerGlu	195
Db	2383	GCGTGTGCCCTCTGAGGACAGAACGAGAAAGGAGAAGGAGCTCCCTGCCCTCTTAAG	2442
QY	196	AlaGluSer-----ThrHisLeuAspThrIleSlysProGly1Tyr-----	208
Db	2443	GCTCTCTAGGCCAGAACGCCAAATGTGGAGACGAGCCCTGAGCATCTT	2502
QY	209	-----AsnGluIleProGluIleArgGluGluAsnGlyGlyAsnGlyAsnThr	221
Db	2503	GCTCTGTCTCCCTGACTGAGGCCAGGCCACCCCAACAGTGGCAGGCCAGGGACT	2562
QY	222	IleGlyThrArgAspGluThrAlaLysGluIalaAspA1aValAspValSerLeuIaGlu	241
Db	2563	AGTGGCTGCCGCAAGCCGAGAACGAGCAAGGCCAAAGACGACTCCATTG	2622
QY	242	GlySerIasnAspIleMetGlySerThrAsnPhenLysGluIleuProGly1ArgGluGlyAsn	261
Db	2623	CCTTGAGAGAACCAAGCTGCTCTACCGCTCAGGAGAACGGAACTCTCCCAACAAAGCTTG	2682
QY	262	ArgVal-----AspAlaGlySerGlnAsnAla	270
Db	2683	ATGGTGAGATCACCTAGACCTGCTCTCGGATACCCAGCCTCCGGAAAGGGAGC	2742
QY	271	HisGlnGlyLysValGluPheHistY-ProProAlaProSerIysGluIysArglySglu	290
Db	2743	CGCCAGGGAAAGCAGAGATAAACAGCCGGCAGGAAAGGACACGCTCTGAAGAG	2802
QY	291	GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly	310
Db	2803	ACGAGCTCACAGCTCA-----AGCAACTTGGCCAAGAGAGAAAGGGT	2847
QY	311	SerThrArgLysGlyValAspIleSerAsnArgAsnGlnAlaThrLeuAsnGly	330
Db	2848	GAAGGAGAAAGAGACTGTGAT-----ACAAGAAATACT	2880
QY	331	ArgPheProSerIysGlyLysSerGluIleProSerArglyLeuAspAsn	350
Db	2881	AGA-----CTGGAGAAG	382
QY	351	GluIleIysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThr	369
Db	2893	GAAATCAAAATCACAGTCATCTTCATCTCCACAAATACTCTAAACAAAG	2952
QY	370	-----HisGlyArgLysIstYrHistYrValProHisArgGlnAsn	382
Db	2953	CCCTCAGGCCCTCTACGTCTCAAAAGGAAATACTGCTCCCCGCCACCGTGTGCC	3012
QY	383	AsnSerThrArgAsnIysGlyMetProGlyIysGlySer-----	396
Db	3013	TGTCCTCCAGAAGGCCAGCTCAAGCTGACTTAAGAGCTCAAGGGAAAGGACACC	3072
QY	397	TrpGlyArgGlnPro-----HisSerAsnArgArgPheserSer	409
Db	3073	TGTGCGCAGAACCCCTCCAAAGGACTTCAAGGAGAACGACCAAGACTCTTC	3132
QY	410	ArgArgArgAspAspSerSerGluSerAspSerIleSerSerGlu-----	426
Db	3133	ATTCGAAAGCAGAGAGAGTAGAGGGAAGGGCTCAGGAAGCTCGGACCAAGGGT	3192
QY	427	SerAspGlyIysP	430
Db	3193	TCTTCGGAGAT	3204

2644 CCTTTGAGAGACAAGGAGACAAAGGAGACACTCTCCCTCAGGGAGACTCTCCCCACAAAGCTTG 2703
 QY 262 ArgVal----AspAlaGlySerGlnAsnAla 270
 DB 2704 ATGGTGAAGATCACCTAGACCTGCTCTCGGATAACCCAGCCTCCGGAAAGGGGAG 2763
 QY 271 HisGlnGlyLysValGluHeHisTyrProProAlaProSerLysGluAspGlySerGlu 290
 DB 2764 CGCCAGAGGAAGAGAAAGATAAACAGGCCCGGAGAAAGAGCAACGCTCTGAGAG 2823
 QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGlyLysGly 310
 DB 2824 AGGAATCTGGCAAAAGAGAAAGCT 2868
 QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
 DB 2869 GAGCCAGAAAGAGAGACTGAT 2901
 QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProSerArgGlyLeuProSerArg 350
 DB 2902 AGA----AspAlaGlyLeuProSerArgGlyLeuAspAsn 350
 DB 2902 AGA----AspAlaGlyLeuProSerArgGlyLeuAspAsn 350
 Alignment Scores:
 Prod. No.: 0.00501 Length: 9391
 Score: 137.00 Matches: 100
 Percent Similarity: 34.70% Conservative: 61
 Best Local Similarity: 21.55% Mismatches: 192
 Query Match: 6.01% Indels: 113
 DB: 5 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-25 (1-9391)
 QY 37 AlanineSerLysLeuHisAspGlnGluLutyrGlyAlaAlaLeuLeuArgAsnAsnMet 56
 DB 1959 GCAAGCTGACAATGTGCTGACCAAGTGCCAGCAGCTGCCCAG 2018
 QY 57 GluHisIleMetGlyProValThrAlaIleLeuGlyGluGluAsnLysGluIleAsn 76
 DB 2019 GAGCAC----AGAGCCCCACGGGAGACAGAGTAAGGGGAGACGTGGCAC 2075
 QY 77 ThrProArgAsnValLeuAsn----IleIleProAlaSerMetAsnTyraAlaYsAla 94
 DB 2076 GACTC-ACGAGCATTCTGAATCCAAGAATCTCTCCCTC-----CTAAAGCT 2119
 QY 95 HisSerLysAspLysLysProGlnArg----AspSerGlnAlaGln 109
 DB 2120 CC-AGCAAAGCCCCCGGGCCOACCCGAAAGGGAGCTCCAGACTTCAG 2178
 QY 110 LysSerProLysSerLysSerIleAspTyrlLeuLys 129
 DB 2179 AAGTCCTGGACAGCAGGGAGCCCCCAAAAGCCTAACACCCCAA 2238
 QY 130 HisLeuUserLysValLysLysProSerAspPheGluGlySerGlyTyrrThrAspIle 149
 DB 2239 -----AACCCTCTCAAGGCTCTGGGAGGGTCAAGGACAGCAACCCCAA 2283
 QY 150 GluGluLysGlyAspAsnAspLysProPheSerLysLysProGlyGinProGlyLysAsp 169
 DB 2284 CAGGGGAAAGGGGACGGGCTTCTCCCTATGGCTCCAGACACTTCAGAGAC 2343
 QY 170 IlePro-----GlyLysGlyGlu----- 175
 DB 2344 AAGCCCAAGGTGAAGGAGAAAGGACCGCCGGGAGGGCTCCCTGCCCCCTTAAG 2463
 QY 176 AlanThrGlyProAspIleGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
 DB 2404 GCAGTCCTCTCAAGCCCAAGAAATGGAGAACGAGCAATGGGAGACAGGAGCTT 2523
 QY 196 AlaGluUser-----ThrHisLeuAspThrLysProGlyTyrr---- 208
 DB 2464 GCTCTCTCAAGCCCAAGAAACCCGAGAACGGAGCAATGGGAGACAGGAGCTT 2523
 QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
 DB 2524 GCTCTTGTCTCCCTGAGGAGCAACGGGACAGTCAGTGGCAGCAGACT 2583

RESULT 13
 PCT-US94-04496-25
 Sequence 25, Application PC/TUS9404496
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 APPLICANT: Canaan, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz &
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:
 CLASSIFICATION:

Qy 2222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaIleValAspValSerLeuValGlu 241
 Db 2584 AGTGCTGCCAGCCAGGCCAGGGAGACAGGGCAAGACGACTCCCATG 2643
 Qy 242 GlySerAsnAspPileMetGlySerThrAsnPhenylsGluLeuProGlyArgGluglyAsn 261
 Db 2644 CCTTGAGGAGACCAAGTGCTCACCGCTCAGGAACTCTCCCAACAAAGCTTG 2703
 Qy 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
 Db 2704 ATGGTGAAGATCACCTAGACCTGCTCTCGGATAACCCAGGCCCTCCGGAGGGCAG 2763
 Qy 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluArgLysGlu 290
 Db 2764 CGCCAGAGGAARGAGAGATAAACAGCCGCCAGGGAAAGAGCAGCAGCTGAGAG 2823
 Qy 291 GlySerSerAspAlaAlaLysSerThrAsnTyrAsnGluIleProLysGlyLysGly 310
 Db 2824 AGGAAGCTCGACAGCTCA-----AGCACTTGGCCAAGAGAAAGGCT 2868
 Qy 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
 Db 2865 GAACAGAGAGAGACTGAT-----AACAGAAATAC 2901
 Qy 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProSerArgGlyLeuAspAsn 350
 Db 2902 AGA-----CTGGAGAG 2913
 Qy 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleLeuThr-- 369
 Db 2914 GAATCAAAATCACAGTCATCTCATCTCATCTCATCTCATCTAAACAAAG 2973
 Qy 370 -----HisGlyArgLysTyrHistYrValProHisArgGlnAsn 382
 Db 2974 CCTCCAGGCCCTCTCAAGCTCTCCACACCGTGTCA 3033
 Qy 383 AsnSerThrArgAsnLysGlyMetProGlyGlySer----- 396
 Db 3034 TCGTCCTCCAGAGCCAAAGCTTAAGAGCTCAAGGGCGGAAAGGAGAACAC 3093
 Qy 397 TrpGlyArgGlnPro-----HisSerAsnArgPheSerSer 409
 Db 3094 TGTCGCCAGACGCCCTCCAAAGTGGCCAGCTACCAAGAGCAACCAAGACTCTC 3153
 Qy 410 ArgArgArgAspSerSerGlySerSerGlySerSerGlu----- 426
 Db 3154 ATTCCCAAGCAGGAGAAAGCTCCAGGAGCTCCAGAGCAACAGGT 3213
 Qy 427 SerAspGlyAsp 430
 Db 3214 TCTTCCGGAGAT 3225

RESULT 14
 US-08-568-459A-1
 ; Sequence 1, Application US/08568459A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chitnis, Chetan
 ; APPLICANT: Miller, Louis H.
 ; APPLICANT: Peterson, David S.
 ; APPLICANT: Su, Xin-Zhuan
 ; APPLICANT: Wellens, Thomas E.
 ; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM ERYTHROCYTE BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Knobbe Martens Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92660

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-568,459A
 FILING DATE: 07-DEC-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned
 REGISTRATION NUMBER: 29-655
 REFERENCE/DOCKET NUMBER: NIH121.001CP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4084 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium vivax
 US-08-568-459A-1

Alignment Scores:
 Pred No.: 0.00256 Length: 4084
 Score: 134.50 Matches: 97
 Percent Similarity: 36.42% Conservative: 80
 Best Local Similarity: 19.96% Mismatches: 220
 Query Match: 5.90% Indels: 89
 DB: 2 Gaps: 21

US-09-700-696C-2 (1-430) x US-08-568-459A-1 (1-4084)

Qy 2 AspLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIle 21
 Db 1724 AATAATTCAATAGTGTAAAACGAGAAAACGTTCAAGACGGCAGGTATCGTAACCTCT 1783
 Qy 22 TyrProlySSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLysIle 41
 Db 1784 TAT-----GATATACTAAACAG--- 1801
 Qy 42 HisAspGlnGluLysTyrGlyAlaAlaLeuIleArgAsnAsnMetGinHisIleMergly 61
 Db 1802 ---GAGTGTAGTAAATTAAACGAGCTTGTGAGATGAAATTAAACACTGTATGT 1858
 Qy 62 ProValThrAlaIleLysLeuLeuGly-----GluGluAsnLysGluAsnThrProArgAsn 80
 Db 1859 GCATATATTGAGTTATGGTTGTTGGTGTGAGAGCTTAAAGAAATACTCGGAAGTT 1918
 Qy 81 ValLeuAsnIleLeProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
 Db 1919 GTGACACATGTGACATGCTAAATCTCAGGCC---ACCAATTCAAATCGGATAAGT 1975
 Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerThrHisArg 120
 Db 1976 CAGCCCTCTAGTAGTACTAAACGGAAAGGTCCA-----GGGAAATTCAAGCT 2026
 Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysVal---LysLysIleProSer 139
 Db 2027 ----CGAATGTTACAGGCCAGATGTTACACAGGTAAGCTGTTACGGGG 2080
 Qy 140 AspPheGluGlySerGlyTyrThrLeuGln-----GluGlyGlyAspAsnAsp 156
 Db 2081 GATGGCTAAATGGAAATCAGACCTGCAAGAAAGGATGTAACGGAAACTGATATGGCC 2140
 Qy 157 IleSerProPheSerLysAspGlyGlnProGlyLysAspIleProGlyLysGlyGlu--- 175
 Db 2141 GAAAGGTAAAGTCGTTAAATGCTGAAATCTGTAAGTAAAGAGTGCAGGAC 2200

Qy 176 -----AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGly 192
 Db 2201 ACTGCAAAGGTTAACGGTATTGCGAAAGCTGGAAAGGA---AACTTGGCCATCAAT 2257
 Qy 193 ProSerGluAlaGluSerThrHisLeuAspThrLysLysProGly----- 207
 Db 2258 AGTCGACCTTCAGTCCACC---GTTGAGCCAATAGCCAGGTGATGATACTGTGAAAC 2314
 Qy 208 -----TyrAsnGluIle 211
 Db 2315 AGTCATCTATACTCTAGTGAATGGTCAAAACCATGTTAACCCCTATAATGGTTG 2374
 Qy 212 ProGluLysGluGluAsnGlyGlyAsn-----Thr 221
 Db 2375 AGCCATTGGAAAGCAATAGTGAATGGCTGCAATGGGATCCGAT 2434
 Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
 Db 2435 TCAAATAGTAAAGTCAAGCAGCGAAAGGGCAAGATAATGATAATGCCAAGGCTACTAA 2494
 Qy 242 GlySerAsnAspIleMetGlySerThrAsnPhenylAspGluLeuAspProGlyArgGluGly 261
 Db 2495 GATACTACTAAATGGTCAGATGTTACCGC-----TCCTACGGGTGAT 2539
 Qy 262 ArgValAspAlaLysGlySerGlnAsnAlaHisGlyLysValGluPheHistyrProPro 281
 Db 2540 ACTACTATGGACTGTGAAATTAATGGTTCTGAGGTAGGGATAAACT 2599
 Qy 282 AlaProSerLysGluLysGluLysSer-----AspAlaAlaGluSer 298
 Db 2600 GTAGGAGTAAGATGAGGAGGGGGAGATACTTGAAATAAAGGTGACGACTGTAA 2659
 Qy 299 ThrAspThrAsnGluIleProLysAsnGlyLysGlySerThr-----ArgLysGly 315
 Db 2660 GTTGGTGAGGATAATTGGTGAACAGCCGGGGAGATACTTGAAATAAAGGTGACGACTGTAA 2719
 Qy 316 ValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArg-----PhePro 333
 Db 2720 AATGACACGGAAAAAGAACGGGSCCTAACCTGACAGTAACAAACTGAGCATGCACT 2779
 Qy 334 SerLysGlyLysSerGlnGlyLeuProSerArgGly-----LeuAspAsnGlu 351
 Db 2780 GGCTTAAGTAAACCGAAAGTTAGAATCAACAGAAAGTGGAGATAGAACTTAATGAT 2839
 Qy 352 IleLysAsnGluMetAspSerPheAspGlyProSerHisGluAsnIleIleThrHisGly 371
 Db 2840 ACAAATCAACGTTAGAAATAAAAATGGAGAAAAGAAAGGATATGAT 2899
 Qy 372 ArgLysGlyHistyrValProHisArgGlnAsnAspSerThrArg----- 386
 Db 2900 TTAAAGATGAAATGCAAGCCGAAATGAGAACAAACTCTGACAGTAACAACTGAGCA 2959
 Qy 387 -----AsnLysGlyMetProGlnGlyLysGlySerTyrPheArgGlnProHisSer 403
 Db 2960 GGACATGACAGGATAGCATCAAATGATAAACAGGATATGAGCAAA 3013
 Qy 404 AsnArg---ArgPheSerSerArgArgAspAspSerSerGluUserSerAspArgGly 422
 Db 3014 ATAAGATACCTTTACGAAAAAATAACAAATAGTCACATTAAATGATAATTTG 3073
 Qy 423 SerSerGluSerAsp 428
 Db 3074 ACTAACTGAAATAATTAGAT 3091

Qy Peterson, David S.
 Su, Xin-zhuan
 Applicant: Wellens, Thomas E.
 Title of Invention: BINDING DOMAINS FROM PLASMODIUM VIVAX
 Number of Invention: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 Correspondence Address:
 Addressee: Knobbe Martens Olson & Bear
 Street: 620 Newport Center Drive 16th Floor
 City: Newport Beach
 State: California
 Country: US
 Zip: 92660
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patent-in Release #1.0, Version #1.25
 Current Application Data:
 Application Number: US/08/487,826B
 Filing Date: 10-SEP-1993
 Classification: 435
 Attorney/Agent Information:
 Name: Israelson, Ned
 Registration Number: 29,655
 Reference Document Number: NIH121.001CP1
 Telecommunication Information:
 Telephone: (619) 235-8550
 Telefax: (619) 235-0176
 Information for SEQ ID NO: 1:
 Sequence Characteristics:
 Length: 4084 base pairs
 Type: nucleic acid
 Strandness: single
 Topology: linear
 Molecule Type: DNA (Genomic)
 Hypothetical: NO
 Original Source:
 Organism: Plasmodium vivax

US-08-487-826B-1

Alignment Scores:
 Pred. No.: 0.00256
 Score: 134.50
 Percent Similarity: 36.42%
 Best Local Similarity: 19.96%
 Query Match: 5.90%
 DB: 2
 DB: 220
 DB: 80
 DB: 220
 DB: 97
 DB: 220
 DB: 80
 DB: 220
 DB: 99
 DB: 21
 DB: 1784 TAT-----GATTAATCAAACAG-----GATTAATCAAACGTTGATGTT 1801
 Qy 42 HisAspGlnGluGluTyrGlyAlaAlaLeuIleAsnAsnMetGlnHisIleMetGly 61
 Db 1724 AATTAATTCATAAAGTAAATACGAGAAAGGTAGACGGCAGGTATCTAAATRCCT 1783
 Qy 22 TyrProLyssSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeu 41
 Qy 2084 TAT-----GATTAATCAAACAG-----GATTAATCAAACGTTGATGTT 1801
 Qy 62 ProValThrAlaIleLeuIleGly---GluGluAsnThrProArgAsn 80
 Db 1859 GCAATATTGAGTTAGCTGTTGTTGCTGTTGAGGCTAAATACGAGAGT 1918
 Qy 81 ValLeuAsnIleProLeuSerMetAsnTyrAlaLysAlaHisSerLysAspLys 100
 Db 1802 ---GACTTAGATGAAATTAAACGAGTTGGCTTTGAGAATGAAATGAAACGTTGATGTT 1858
 Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerThrHisArg 120

RESULT 15
 US-08-487-826B-1
 Sequence 1, Application US/08487826B
 Patent No. 593827
 General Information:
 Applicant: Sim, Kim L.
 Applicant: Chitnis, Chetan
 Applicant: Miller, Louis H.

Db	1976 CAGCTGTAGATGTAAGCGGAGAAGTTCCA-----GGAGATTCTACGGAT---	2026	Qy	423 SerSerSerGluSerAsp	428
Qy	121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysVal---LysLysIleProSer	139	Db	3074 AGTATGGAAATTAGAT	3091
Db	2027 -----GAAATGTTAACAGGGCAAGATAGTTCTACACAGGTAACGTTACGGGG 2080				
Qy	140 AspPheGluGlySerGlyTyrrThrAspLeuGln-----GluArgGlyAspAsnAsp	156			
Db	2081 GATGGTCATAATGAAATCAGACACTGGCGAAAGCGATGTACACGAACTGATATTGCC	2140			
Qy	157 IleSerProPheSerLysAspGlyGlnProThrAspLeuGlyGlu---	175			
Db	2141 GAAAGTGTAACTGCTAAATGTTGATTCGAGAAATCTGAAAGTAAAGAAGTACGAC	2200			
Qy	176 -----AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGly	192			
Db	2201 ACTGAAAGGGTACAGTATGCTGAAAGCTGAGGAAAGAA---AACTTACGCGATCAAAT	2257			
Qy	193 ProSerGluAlaGluSerThrHisLeuAspThrLysPheGly-----	207			
Db	2258 AGTCGACCTCTTGACTCCACC---GTTGAGCAAATGCCAACGGTGTACACTGTGAAAC	2314			
Qy	208 -----TyrAsnIleGluGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly	211			
Db	2315 AGTGCATCTATAACCTGTTAGTGTAGTGGTAAAACCCATTGTTAACCCCTATAATGGTTG	2374			
Qy	2112 ProGluArgGluGluAsnGlyGlyAsn-----Thr	221			
Db	2375 AGGCATTCCAAAGCAATAATGCTGATGCGATGCTGGCAATCATGGGAATCTGTGT	2434			
Qy	2222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu	241			
Db	2435 TCAAAATGTAAGGTGAGCGGAAAGGCCAAAGATAATGATAATGCGAAAGGTACTARA	2494			
Qy	2442 GlySerAsnAspIleMetGlySerThrAsnPhenylAspGlyLysGluGlyAsn	261			
Db	2495 GATACTGATTAAGTTCAAGATGGTACCGC-----TCCTCTACGGGTGTT	2539			
Qy	262 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHistyrProPro	281			
Db	2540 ACTACTGATGCCAGTGTATGGAAATTATAAAAGGTGTCTGGGATGGGATAAACCT	2599			
Qy	282 AlaProSerLysGluLysArgLysGluGlySerSer-----AspAlaAlaGluSer	298			
Db	2600 GTAGGAAGTAAAGATGGAGACAGGGGGAAAGATAACCTGCAAAATAAGGATCAGCCACTGNA	2659			
Qy	299 ThrAsnTyrAsnGluIleProLysGlyLysGlySerThr-----ArgLysGly	315			
Db	2660 GTTGCTGAGCATGATGTTGAGACAGGGCTGTGGGACTAAATGATGATCAAAT	2719			
Qy	316 ValAspHisSerAsnArgAsnGlnAlaIthrLeuAsnGluLysGlnArg-----PhePro	333			
Db	27200 AATGACACGGAAAAGAACCGGCCCTACCCCTGACGTAAGAACGAGGATGCAACT	2779			
Qy	334 SerLysGlyLysSerGlnGlyLeuProIleProSerArgGly-----LeuAspAsnGlu	351			
Db	27800 GCGCTTAAGTAAACCGAAAGTTAGATAACAGAAAAGTGAGTAGAACTACTAAATGAT	2839			
Qy	352 IleLysAsnGluMetAspSerPheAsnGlyProSerHistidineSerThrIleThrHisGly	371			
Db	2840 ACAACTAAAGTTAGAAATAAAATGGAGAAAAGCTTACAAAGGATTTACAAAGCATAT	2899			
Qy	372 ArgLysTyrHistyrValProHisArgGlnAsnAsnSerThrArg-----	386			
Db	2900 TTAAAAGTAATGATACGGCAATGAAAGCAAAATTCTGATCAACATGAGTCAGTCAGCA	2959			
Qy	387 -----AsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGlnProHisser	403			
Db	29600 GGACATGAGCAGGGATAGCTCAAAATGATAAAGCAGAA-----AGGAAAGCATATG	3013			
Qy	404 AsnArg---ArgPheSerSerArgArgGlyAspSerSerGluSerSerSpSerDly	422			
Db	3014 AATAAAGTACTTTACGAAAAATAATACAAATAATAGTCACCATTTAAATAGTATAAATG	3073			

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 30, 2003, 00:14:26 ; Search time 423 Seconds (without alignments)

Scoring table: BLOSUM62

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKVEISNKENTHGLRMS.....RRDDSESSSDGSSESSESDGD 430

Scanned: 3349.212 Million cell updates/sec

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=publishedApplications.NA -QMT=fastap -SUFFIX= -MINMATCH=0.1
-LOPCL=0 -LOCPEPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=X=blossum62
-TRANS=human40_cdi -LIST=45 -DOCALIGN=200 -THR SCORE=0.05 THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=doo -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09700696 @CGN_1.221 @runat_26112003_152634_14705
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPPLOC=100
-LOGLOG -TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELEXT=7
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Database :

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Published Applications.NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

1 2276 99.9 1575 12 US-10-311-840-2 Sequence 2, Appli

SUMMARIES

Query No. Score Match Length DB ID Description

1 2276 99.9 1575 12 US-10-311-840-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-10-311-840-2

; Sequence 2, Application US-10311840

; Publication No. US200301175808A1

; GENERAL INFORMATION:

; APPLICANT: KUROKAWA, Tomofumi

; APPLICANT: YAMADA, Takaaki

; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA

; FILE REFERENCE: 2739USOP

; CURRENT APPLICATION NUMBER: US-10/311,840

; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: PCT/JP01/0563

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: JP 2000-191088

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO: 2

; LENGTH: 1575

; TYPE: DNA

; ORGANISM: Human

US-10-311-840-2

Alignment Scores:

Pred. No.: 2.22e-213

Length: 1575

Score:	2276.00	Matches:	429	Db	1246 AGGACCAAGCAACCTAAATGAAAACAAGGTTCTAGTAAGGCCAAAGTCGGC 1305
Percent Similarity:	100.00%	Conservative:	1		
Best Local Similarity:	99.77%	Mismatches:	0		
Query Match:	99.87%	Indels:	0		
DB:	12	Gaps:	0		
US-09-700-696C-2 (1-430) x US-10-311-840-2 (1-1575)					
Qy	1 ValAsnLysGluGlyTyrSerIleSerAsnLysGluAsnThrHisAsnGlyIleArgMetSer 20	Db	341 LeuProIleProSerArgGlyIleAspAsnGluIleSerAsnGluMetAspSerPheAsn 360	Qy	341 LeuProIleProSerArgGlyIleAspAsnGluIleSerAsnGluMetAspSerPheAsn 360
Db	286 CTGATAAAAGAAATAATAGTATCAGTAACAAAGAAATACTACACATGGCTGAGATGTC 345	Db	1306 CTGCCCCATCCTTCGCGCTGATGATAATGAAATAAACATGGCAAAATACTATTATGAC 1425	Qy	361 GlyProSerIleGluAsnIleLeuThrHisGlyArgLysThrIleSerValProIleSerArg 380
Qy	21 IleTerProLysSerThrGlyAsnGlyIleAspAspAlaIleSerIys 40	Db	1366 GGCCTCCAGTCATGAAATAACATGGCAAAATACTATTATGAC 1425	Qy	381 GluAsnAsnSerIleSerThrArgAlaLysGlyIleSerProGlnGlyIleSerIys 400
Db	346 ATTATCCPAAGTCAACTGGAAATAAGCTTCAACTGGAAATAAGCTCTGGTAGACAA 405	Db	1426 CAATAATTCATCACGGAAATAACGGTAGCCACAGGAAAGGCTCTGGTAGACAA 1485	Qy	401 ProHisSerAsnSerArgPheSerSerArgArgAspSerSerGluSerSerAsp 420
Qy	41 LeuHisAspGlnGluGluIryGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60	Db	1486 CCCATTCACAGGAGGTTAGTCCTCTAGAGGGATGACAGCTAGTCAGTC 1545	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	406 CTATGACCAAGAGAATATGGCAGTCATCATGAAATACATGAACTATGAA 465	Db	1546 AGTGGCACTTCACAGGAGGATGGATGTC 1575	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	61 GlyProValThrAlaIleLysLeuIleGlyGluGluIlyGlyIleAsnThrProArgAsn 80	Db	RESULT 2	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	466 GGGCAAGTCACTGCGATTAACTCTGGGGAAACAAGGAAACACCTAGGAA 525	US-10-311-840-3	Sequence 3, Application US/10311840	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	81 ValIleAsnIleProAlaSerMetAlaSerAlaLysSerIysAspLysLys 100	Db	; Publication No. US20030175808A1	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	526 GTTCTAAACATAAATCCCAGCAAGTATGAAATACTGCTAAAGCAACTCGAAAGGATAAAG 585	Qy	; GENERAL INFORMATION:	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	101 LysProGlnArgAspSerGlnAlaGlnIysSerProValLysSerThrHisArg 120	Db	; APPLICANT: KUBOKAWA, Tomofumi	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	586 AAGCTCAAGAGATTCCAGGCCAGAAAGTCAGAAAGCAAAAGCACCCATGT 645	Qy	; APPLICANT: YAMADA, Takao	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	121 IleGlnHisAsnIleAspItyXleuLysIleSerIysLeuSerIysLysIleProSerAsp 140	Db	; ATTORNEY: MORIMOTO, Shigeto	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	646 ATTCAACAAACATTGACTAACTCTCTAAAGCTAAACATCTCTCAAAAGTC 705	Qy	; TITLE OF INVENTION: No. US20030175808A1	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	141 PheGluGlySerGlyTyrThrAspIleGlnGluArgGlyAspAsnAspIleSerProPhe 160	Db	; CURRENT APPLICATION NUMBER: US/10/311.840	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	706 TTGCAAGGGAAAGCCTTATACAGAACTCTAAAGAGGGACATGATATCTCCCTTC 765	Qy	; CURRENT FILING DATE: 2002-12-18	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	161 SerGlyAspGlyGlnProPheIysAspIleProGlyLysGlyGluAlaIleThrGlyProAsp 180	Db	; PRIORITY NUMBER: PCT/JP01/05223	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	766 AGGGGGGGCCACCTTAAGGATCTCCGTCAGCTGTCTGAC 825	Qy	; PRIORITY FILING DATE: 2001-06-20	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyIleProSerGluAlaGluSerThrHis 200	Db	; PRIORITY APPLICATION NUMBER: JP 2000-191088	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
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Db	886 CTGTACACAAAAGCCAGGTTATAATGAGATCCAGAGAAAGAAATGTTGGAAAT 945	Db	; SEQ ID NO: 3	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	221 ThrIleGlyIysAspIleGlnThrGlyPheAlaGlyIleProSerGluAlaIleSerLeuVal 240	Db	; LENGTH: 1662	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	946 ACCATGGACATGGGATGAAACTGGCAAGGCAATGGCAAGCTGAGTGAATGTA 1005	Db	; TYPE: DNA	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	241 GluGlySerAsnAspIleMetGlySerThrAsnPhelysGluIleProGlyIleArgGluGly 260	Db	; ORGANISM: Human	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
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Qy	261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValAspHisSerAsn 280	Db	Qy 1 ValAsnIyGluGlyTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
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Qy	281 ProAlaProSerLysGluIysAspGlyLysGluIleProSerAspAlaAlaGluSerThrAsn 300	Qy	Qy 21 IleTyrProLysSerIleGlySerIleLeuIleGlyGluGlyIleSerIleSerLys 40	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Db	1126 CCTGCACCTCAAAGAACAAAGAACAAAGGAGTAGTGTGAGCTGAGTCACATAATG 472	Db	Db 413 CTACATGACCAAGGAAAGTAACTCCCTGGGAACTACCTGGGAAAGAACACCTGAAAT 472	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
Qy	301 TyrAsnGlnIalThrLeuAsnGluLysGlnArgPheProSerLysGlyIysSerGlnGly 340	Db	Qy 61 GlyProValThrAlaIleLeuIleGlyGluGluIlysGluAsnThrProArgAsn 80	Qy	421 SerGlySerSerSerGluSerAspGlyAsp 430
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; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 33
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-794-422-33
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Qy 121 IleGlnHisAsnLeAspTyrLeuLysSerIleSerLysValLysIleProSerAsp 140
Db 653 ATTGACACATGACTAACATCTCAAAGTCAAAAAATCCCAGTGT 712
Qy 141 PheGluGlySerGlyTyrThrAspLeuGluArgGlyAspAsnAspIleSerProPhe 160
Db 713 TTGAGGGCGGTATACAGATCTCTAGAGAGGAGCATGATATACTCTCTTC 772
Qy 161 SerGlyAspGlyGinProPhyLeAspIleProGlyAsp 180
Db 773 AGTGGGAACTCTTAAGACATTCCTGTAGAGAGCTGTCCTGAC 832
Qy 181 LeuGluGlyLysAspIleAspIleGlnThrGlyPheAlaGlyProSerGluA1aGluSerThrHis 200
Db 833 CTAGAGGCAAGATTAAACGGGTGAGCCAGTGAAGCTGACTACTA 892
Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGluGlyAsn 220
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Qy 221 ThrIleGlyThrAspGluThrAlaLysGlnAlaAspAlaValAspValSerLeuVal 240
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Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrrAlaLysAlaHisSerLysAspIleGly 60
Db 478 GRTCTAACATATCCAGCAAGTAAATTATGCAAACTGCAACACTGAAAGATAAAAG 477
Qy 101 LysProGlnArgAspSerGlnAlaGlnIleSerProValLysSerThrHisArg 120
Db 538 AAGCCCTCAAGAGGATTCCTCAAGGCCGAAAGTCCGTAAAAGGACCAATCGT 597
Qy 121 IleGlnIiisAspIleAspTyrrAspIleSerLysValLysIleProSerAsp 140
Db 598 ARTCAACACACATTCGCAAGTAACTGCAAACTGAACTGAAAGATAAAAG 657
Qy 141 PheGluGlySerGlyTyrThrAspLeuGluIleGlyAspAsnAspIleSerProPhe 160
Db 658 TTGAAAGCAGGGTATAAGATCTCAAGAGAGGGCAATAATATCCTTC 717
Qy 161 SerGlyAspGlyGlnProPhyLeAspIleProGlyLysGlyIleGluIleGlyProAsp 180
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US-09-794-422-33

QY 201 LeuAspThrLysProGlyTyraSerGluileProGluArgGluGluAsnGlyGlyAsn 220
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QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
 Db 898 ACCATGGAACTTGGATGAAACTCGAAAGGGAGATGCTGTTGATCTGCTTGTCA 957

QY 241 GluGlySerAsnAspIleMetGlySerThrAsnHeLysGluLeuProGlyArgGluGly 260
 Db 958 GAGGCCAGAACGATATCATGGTAGTACCAATTAAAGGTCCTCGAGAGAAGGAA 1017

QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
 Db 1018 AACAGAGTCGATGTGGCACAAATGGTCACCAAGGGAAAGGTGAGTTCAATTACCT 1077

QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluUserThrAsn 300
 Db 1078 CCTGACCTCAAAGAGAAAAGAGGCGCTAGTGATGTAGCTAAAGTACCAAC 1137

QY 301 TyrAsnGluileProLysSerGlySerGlySerThrArgLysGlySerSerAsn 320
 Db 1138 TATATGAAATTCTAAATGGCAAGGCGTACCAAGGAAATCTTCAAT 1197

QY 321 ArgDnsGlnAlaThrLeuIleGlyLysGlySerGlyLysGly 340
 Db 1198 AGGAAACAGCAACCTTAATGAAAGAAAGTTCCTAGTAAAGGCAAAATCTTCAAT 1257

QY 341 LeuProIleProSerArgIleGluAspArgPheProSerLysGlySerGly 360
 Db 1258 CTGCCCATCTCTTCGTTGCTGTATGAAATCAAAACGAAATGGATTCTTCAAT 1317

QY 361 GlyProSerThrGluAsnBillerleThrIleGlyArgLysTyrHistYValProHisArg 380
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QY 381 GluAsnAsnSerThrArgAsnLysGlySerTrpGlyArgGln 400
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QY 421 SerGlySerSerGluUserAspGlyAsp 430
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RESULT 4
 US-09-794-422-45
 ; Sequence 45, Application US/09794422
 ; GENERAL INFORMATION:
 ; CURRENT APPLICATION NUMBER: US/09794422
 ; PUBLICATION NO.: US20030166239A1
 ; APPLICANT: Brown, Thomas A.
 ; DE WET, Jeffrey R.
 ; PRIORITY: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445
 ; CURRENT APPLICATION NUMBER: US/09794422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIORITY: 2000-02-19
 ; PRIORITY NUMBER: 60/185,617
 ; PRIORITY FILING DATE: 2000-02-19
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 45
 ; LENGTH: 1969
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ;
 US-09-794-422-45
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Db	US-09-794-422-7	1641	AGTGGCAGTTCAGTGGAGCGATGGTGCAC	1670
SEQUENCE LISTING				
Sequence 7	Application US/09794422			
PUBLICATION NO.	US20030166239A1			
GENERAL INFORMATION:				
APPLICANT:	Brown, Thomas A.			
De Wet, Jeffrey R.				
APPLICANT:	Gowen, Lori C.			
APPLICANT:	Hames, Lynn M.			
TITLE OF INVENTION:	Mammalian Osteoregulins			
FILE REFERENCE:	PC10445			
CURRENT APPLICATION NUMBER:	US/09794,422			
CURRENT FILING DATE:	2001-02-27			
PRIOR APPLICATION NUMBER:	601185,617			
PRIOR FILING DATE:	2000-02-29			
PRIOR APPLICATION NUMBER:	601234,500			
PRIOR FILING DATE:	2000-09-22			
NUMBER OF SEQ ID NOS:	46			
SEQUENCE TYPE:	Patentin Ver. 2.0			
SEQ ID NO:	7			
LENGTH:	2112			
ORGANISM:	Homo sapiens			
JS-09-794-422-7				
Alignment Scores:				
Pred. No.:	3.25e-213	Length:	2112	
Score:	2276.00	Matches:	429	
Percent Similarity:	100.00%	Conservative:	1	
Best Local Similarity:	99.77%	Mismatches:	0	
DB Query Match:	99.67%	Indels:	0	
DB Query:	12	Gaps:	0	
US-09-700-698C-2 (1-430) × US-09-794-422-7 (1-2112)				
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Db	474 CTGATAAAAGAATAATAGTATCGTAAAGATACTCACATGGCTGAGATGTC 533			
QY	21 IleTyrProLysSerThrGlyAsnLysGlyIleProGluAsnGlyIleAspSerIleSerIys 40			
Db	534 ATTTATCCAAAGTCAACTGGAAATAAGCTTGGAGATGATGATCCTATCGCAA 593			
QY	41 LeuHisAspGlnGluLysGlyIleAlaLeuIleArgAsnMetGlnHisIleMet 60			
Db	594 CTACATGACCAAGAGAAATAATGGCCAGCTCTCATCAGAAATACATGGAAACATATAATG 653			
QY	61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80			
Db	654 GGGCAGTGTGACTGCATTAACTCTGGGGAGAAACACCTAGGAT 713			
QY	81 ValLeuAsnIleProIleSerMetAsnIleIleAlaHisSerIysAspIysLys 100			
DDB	714 GTTCTAAACATAATCCAGAAAGTGAATTATGCTAAACATCGAGGATAAAAG 773			
QY	101 LysProGlnIargAspSerGlnAlaGlnIlySerProValIysSerThrHisArg 120			
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QY	121 IleGlnHisAsnIleAspTyrIleSerIlysIleProSerAsp 140			
DDB	834 ATTCAACACATTCACCTAAACATCTCTCAAACACTCCTGAT 893			
QY	141 PheGluGlySerGlyTyrThrAspLeuGlyGluArgGlyAspAsnIleSerProIle 160			
Db	894 TTGAGGGCACGGTATACAGATCTTACAGGCAAGATACTCCTTC 953			
QY	161 SerGlyAspGlyGlnProPhoLeuAspIleProGlyLysGlyIleGluAlaThrGlyProAsp 180			
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RESULT	7			
US-09-794-422-3				
Sequence 3, Application US/09794422				
Publication No. US20030166239A1				
GENERAL INFORMATION:				
APPLICANT: Brown, Thomas A.				
APPLICANT: De Wet, Jeffrey R.				
APPLICANT: Gowen, Lori C.				
APPLICANT: Hames, Lynn M.				
TITLE OF INVENTION: Mammalian Osteoregulins				
FILE REFERENCE: PC10445				
CURRENT APPLICATION NUMBER: US/09/794,422				
CURRENT FILING DATE: 2001-02-27				
PRIOR APPLICATION NUMBER: 601185,617				
PRIOR FILING DATE: 2000-02-29				
PRIOR APPLICATION NUMBER: 601234,500				
NUMBER OF SEQ ID NOS: 46				
SOFTWARE: PatentIn Ver. 2.0				
SEQUENCE ID NO. 3				
LENGTH: 1682				

;

TYPE: DNA
ORGANISM: Mus musculus
US-09-794-422-3

Alignment Scores:
Pred. No.: 1.06e-86
Score: 983.50
Percent Similarity: 62.16%
Best Local Similarity: 50.47%
Query Match: 43.15%
DB: 12

US-09-700-696c-2 (1-430) x US-09-794-422-3 (1-1682)

Qy 6 SerileSerAsnlysGluAsnThrHisAsnGlyLeuArgMetSerileTyrProLyser 25
Db 165 AGCTCGGGATTCAGACGATTCAAGGACTTCAAGGACTTGGGATCTGTGATCC 225
Qy 26 ThrGlyAsnlysPheGluAspGlyAspAspAlaIleSerLeuHisAspGlnGlu 45
Db 226 ACGGTGGATAGGAGACAGGGATGGCAAGGGCTCTTACCCGGCTGCGGAC 285
Qy 46 GluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAla 65
Db 286 AGGTATGGTGTGCTCCAGAAATATACGGCCTGTAAGAGTGTAGGACTGG 345
Qy 66 IleLeuLeuGlyGluGluAsnlysGluAsnThrProArgAsnValLeuAsnIleIle 85
Db 346 GCGGAACTACGGGAAACAGGGAAAGACCTCAGACTGTTAACGGTATT 405
Qy 86 ProAlaSerAspTyrAlaLysAlaHisSerLysAspLysLysProGlnGlyAsp 105
Db 406 CCAGCAGATGTCAAATGATGCTAAACTCTCTAAAGACATAAGAAGAGTT 465
Qy 106 SerGlnAlaGlnIleSerProValIleSerLysSerLysThrArgIleGln 122
Db 466 CTGGCTAACCCAGAGCCGGTCAAAGCAAAACACACCAAAACACCCGCAAGCCGA 525
Qy 123 HisAsnIleAspTyrLeuIleSerLysIleSerLysIleProSerAspPheGlu 142
Db 526 CGGAGGACTACTGAGACATCAGAACATCAGAACATCAGAACATCAGCTTCAA 585
Qy 143 GlySerGlyTyrThrAspIleGluArgGlyAspAsnAspIleSerProHeSerGly 162
Db 586 GGCAGTGCTGCCAGATCTCTAGTGAAGGAGTATGATGTCGCCCTTCAGTGA 645
Qy 163 AspGlyGlnProPhylAspIleProGlyLysGlyGluAla--ThrGlyProAspIle 181
Db 646 GATGGCAACATTTATGACATTCCTGGAAAGAGGCTGCTGAGTCTCTGAA-- 702
Qy 182 GluGlyLysAspIleGlnThrGlyPheAlaGlyProSerLysAlaGluSerThrHisLeu 201
Db 703 ----AGCTCAACTAGTCGCCCCCTCTAGGTCAAGCTAACGTTATGACCA 756
Qy 202 AspThrLysSlysProGlyTyrAsnGluIleProGluArgGluGluAsnThr 221
Db 757 CATATGAGTGCAGTGGCTTAATGAGATCCGGGAGAGGACATGTGGCAGTGGC 816
Qy 222 IleGlyThrArgAspGluThrAlaAspAlaValAspValSerIleValGlu 241
Db 817 TATGCAACACAGAACAGCAAGCTGCAAGGGCCAGCTGCGAGCTGCTGCGAGA 876
Qy 242 GlySerAsnAspIleMetGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsn 261
Db 877 GCGAGGATGAAATCACAGGCACTTCAGGCAACTCCCGGAAGAGGAAAC 916
Qy 262 ArgValAspAlaGlySerGlnAlaHisGlnGlyLysValGluPheIstTyrPro 281
Db 937 AGAATTAATGCGGCCAGCAAAATGTCTATCAAGGAAAGTGTACTATCCAA 996
Qy 282 AlaProSerGlySerGlyAspLysGluGlySerSerAspAlaAlaGluSerThrAsnIle 301
Db 997 GGGCCCTGAGAGAAAAGCTAAAGGAGCTGGGGTGGAGCATCAGGGAGA 1053
Qy 302 AsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArg 321
Db 1054 AACGAAATCCCAGGGCAAGCTAGCTCTAAAGATGCCAGAGGG 1113
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Db 1114 ACCCAATAACCTTGACTGCAAGGAAAGATTCCAGTAAGGCAAAAGCCAGGGCCCT 1173
Qy 342 ProIleProSerArgGlyLeuAspSerGluMetAspSerPheAsnGly 361
Db 1174 GCTCTGCCCTCAAGCTTAGATGAGTAAAGTGA----- 1215
Qy 362 ProSerHisGluAsnIleThrHisGlyArgLysTyrHisIleThrValProHisArgGln 381
Db 1216 -----GAAAC-----CATTAGTGTCATGGACAA 1242
Qy 382 AsnAspSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyr--GlyArgGln 400
Db 1243 AATAATCTTACACGGATAAAGGGATGTCACAGCAGAGGCTCCTGGCCTTCGAGAAGA 1302
Qy 401 ProHisSerAsnArgPhesSerArgGlyAspPheSerGluSerSerAspTyr 420
Db 1303 CCCAAATCCCCACAGGGCGCTAGCACCCGCAAAAGA--GACAGCAAGCAGTCGTCATCC 1359
Qy 421 SerGlySerSerSerGluSerAspGlyAsp 430
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RESULT 8
US-09-794-422-1
Sequence 1: Application US/09794422
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPICANT: Brown, Thomas A.
; APPICANT: De Wet, Jeffrey R.
; APPICANT: Gowen, Lori C.
; APPICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIORITY APPLICATION NUMBER: 60/185,617
; PRIORITY FILING DATE: 2000-02-29
; PRIORITY APPLICATION NUMBER: 60/234,500
; PRIORITY FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1
Alignment Scores:
Pred. No.: 2.66e-82
Score: 938.50
Percent Similarity: 59.95%
Best Local Similarity: 49.41%
Query Match: 41.18%
DB: 12
Length: 1655
Matches: 211
Conservative: 45
Mismatch: 146
Indels: 25
Gaps: 8
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Db 146 AACAAAGCCAAATATCAGC-----TTAGCATGCTGAGCCCATGGGCGGT 196
Qy 29 LysGlyPheGluAspGlyAspAspAlaIleSerIleLeuHisAspDlnGluGly 48
Db 197 AACGGAAACAGGGTGGCGAGATGGCTCCCTGCACTGCTGAGCAGCAAC 256
Qy 49 AlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLeu 68

Qy 144 rglytyrthrAspIeuGlnGluArgGlyAspAsnAspIleSerProHeserGlyAspI 164 ; PRIORITY NUMBER: US 09/387,462
 Db 5664 AGAGATGATGAACTGATAGCAGCATCAGACACTAACTATAGTGACAGTCATGCCAATG 5723 ; PRIORITY FILING DATE: 1999-09-01
 Qy 164 yGlnProPheIysAsp-----IleProGlyLysGlyGluAlaIthrGlyPr 179 ; PRIORITY APPLICATION NUMBER: US 09/145,056
 Db 5724 TAAATGGAAATGATGAAATGAAATCGAGCAGTGCCTAAAGTAAATCAGATAGCAG 5783 ; PRIORITY FILING DATE: 1998-09-01
 Qy 179 oAspIeuGluGlyLysAspIleGlnThrIpheAlaIgLyPrSerGluAlaIgLyPr 199 ; NUMBER OF SEQ ID NOS: 24
 Db 5784 TGACAGTGTAGTAGTGTAGTAGCAGCAATPGCAGTGACAGTCAGACTGACAGTC 5843 ; SOFTWARE: PatentIn Ver. 4.0
 Qy 199 rHiLeuAspIthrLysProGlyTyAspIeuGluIleProGluArgGluGluAsnGlyI 219 ; SEQ ID NO 15
 Db 5844 CAGCAGTATAGAACAGTGGCTGACTGACTGAGTGAGCTGAGTCAGCTGATGATG 5903 ; LENGTH: 5721
 Qy 219 yAsnThrIleGlyThrArgAspIgluThrAlaIlysGluAlaAspAlaValAspIleS 239 ; TYPE: DNA
 Db 5904 CAGGACAGCTGAGTAGTGTAGTAGCAGCAATPGCAGTGACAGTCAGACTGACAGTC 5960 ; ORGANISM: Homo sapiens
 Qy 239 uValGluGlySerAspIleNetGlySerIthrAspIleIgLyGluIleIgLyGlyI 258 ; FEATURE:
 Db 5951 TAGGAGTGAACAGTAGTGTAGTAGTGTAGCTGAGCAGCTGAGCAACTGAGC 6020 ; NAME/KEY: CDS
 Qy 259 -----GluGlyAsnValAspAlaIgLySerGlnAlaIgLyIgLyValI 276 ; LOCATION: (1)...(5721)
 Db 6021 AGAGAGCTCAAGGAGTAGTGTAGCTGACTGACTGAGCAGTCAGCAGTCAGCTG 6080 ;
 Qy 276 upheHistYrProProIaIProSerIysGluIysArgIysGluGlySerAspAlaAl 296 ;
 Db 6081 CAGTAGGCAAAACTGTGAGCGAGAACGACAAATGAGCTAACAGCTGATAGT 6140 ;
 Qy 296 agluSerIthrAspItyAsnGluIleProIysAsnGlyIysGlySerIthrArgIysGly 316 ;
 Db 6141 TGACAGCTGATGAGCTGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 6195 ;
 Qy 316 lAspHisSerAspArgAsnGlnAlaIthrLeuAsnGluIysGlnIargPheProSerIysG 336 ;
 Db 6196 -GACAGCAGCAAAAGCTGAGCATGAGCTGAGCATGAGCTGAGCTGAGCTGAG 6254 ;
 Qy 336 yIysSerGlnGlyLeuProSerArgGlyLeuAsnGluIleAsnGlyIleAsnGly 356 ;
 Db 6255 CAGTGTAGTT-----AGTGAACGGCAGTGATAGTGACAGCTGATAGT 6299 ;
 Qy 356 tAspSerIysAsnGlyProSerHisGluAsnIleIthrHisIgLyArgLyStyHisI 376 ;
 Db 6300 TGACAGCTGATGAACTGAGCAGCAATGAGATGAGCTGAGCTGAGCTGAG 6330 ;
 Qy 376 rValProHisArgGlnAsnAsnSerIthrArgAsnIysGlyMetProGlnGlyIysGly 396 ;
 Db 6331 -----GACAGCAGCAAAAGCAGGATAGCAGTGAACAGCTGAGCTGAGCTGAG 6380 ;
 Qy 396 rTrpGlyArgIysProHisSerAsnArgPheSerSerArgArgArgAsp----- 413 ;
 Db 6381 CAGCAACAGCAGCTGAGCTGAGCATGAGCTGACAGGAAACAGCAGTGAGCTG 6440 ;
 Qy 414 -----AspSerSerGluSerSerAspSerGlySerSerGluSerAsp 428 ;
 Db 6441 TAGCAGTCAACAGCTGATAGTGACAGCTGAGCAACAGCAGTGATGAAAC 6492 ;
 RESULT 10
 US-09-785-770A-15
 ; Sequence 15, Application US/09785770A
 ; Patent No. US2010033601
 ; GENERAL INFORMATION:
 ; APPLICANT: Pan, Yang
 ; APPLICANT: Barnes, Thomas M.
 ; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA - INHIBITING PROTEIN
 ; FILE REFERENCE: 07334-328001
 ; CURRENT APPLICATION NUMBER: US/09/785,770A
 ; CURRENT FILING DATE: 2001-02-16
 ; 1909 GAGATGATGTTGCCAGAGACTGGAAGACAGTT-----CCATTGCGGAGAAATCTT 1965
 ; 166 ProPhe-----LysAspIleProGlyLysGlyIysGluAlaIthrGlyProAspIleGlu 182
 ; 1966 CCCTGCAACACAAAGAAGAGATGTT-----GCTGCACAGCCAGTAAGCAATG 2013
 ; 183 GlyIysAspIleGlnIthrGlyIysGlyIysGluAsnIleAspIleSerProPheSerGlyAspIleGln 165
 ; 2014 AGTGGAGAATAGG-----CTCTCTGAGGGAAGGCCAAGAGCTCTTGGAT 2064

Db	1206	GAGGAGACAGATATGGAGATGAACTGGCCAAACCATGTCATTGAAATCCTACCTC	1265	Qy	23	ProlySerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLysLeuHis	42
Qy	281	-----ProAlaProSerAspGlyAspGlySerGluGlySerAlaAlaGluSer	298	Db	663	CCTGGAAAGGCCAACGCAATGCCGACTGGCCAGACACTGGCCAGAAAGAACAC	722
Db	1266	AGCTATGACCGCCGGAGAAAGAAAGATGTTGAAACT--TGAGCCACGGA	1322	Qy	43	AspGlnGluGluGlyAlaAlaLeuIleArgAsnAsnMetGlnHistileMetGlyPro	62
Qy	299	ThrAsnTyrAsnGluIleProLyAsnGlyGlySerThrArgLySlyValAspHis	318	Db	723	CTGGGTGAAACCCATGGAAAGGGTTTGAGTCAGAACAGGACAC	770
Db	1323	CTTGAGATAAGGACTTAAATGACTCTAAAGGACTGGTAAACTTGACTA	1382	Qy	63	ValThrAlaLleleSleLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeu	82
Qy	319	SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLyGlyLySs	338	Db	770	-----	770
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Qy	339	GlnGlyLeu-----	341	Db	771	-----AAATCTCCACACAGCACAAACGCCGTRG	800
Db	1443	GCCAAAGCTTGAAAGGTGCTGATGTTGCCAGACCTCCCGTACCCGGC	1502	Qy	103	GlnArgAspSerGlnAlaGlnLysSerProValLysSerThrHisArgTleGln	122
Qy	3442	-----ProIleSerArgGlyLeuAspAsnGluIleLysAsnGlu-----	355	Db	801	GATGCCAAAGGTGATGAGAGGGCTCTGNGTGAACAGAGAAATCACAC	851
Db	1503	ATACAGGCCAAATTACCCGTTACACTGCCTTCAGCTCTCCAGCTTCCAGCAAG	1562	Qy	123	HisAsnIleAspIleLeuIysLysIleProSerAspPheGlu	142
Qy	3556	MetAspSerPheAsnGlyProSerHisGluAsn-----	366	Db	852	-----AAGGCCCTCTCCAAA-----	866
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Qy	367	-----IleIleThrHisGlyArgIleGlySerIleValPro-----	378	Db	867	-----GAGGAAACCCAGGGCACCCCTAGGG	893
Db	1623	AATTCCAAGATGCACTGTTCTCAAGTGTCTCCATCTCCCTAAATGATGAC	1682	Qy	163	AspGlyGlnProPheLysAspIleProGlyLysGlyGluIalThrGlyProAspLeuGlu	182
Qy	379	--HisArgGln 381	-----	Db	894	GACAATGCCAGGAAACCG--CCCTCTAGGGCTAAAGGAAAGAGAGAGAGAG	950
Db	1684	TTGACCAACCAA 1694	-----	Qy	183	GlyIysAspIleGlnThrGlyPheAlaGlyProIleGluUser--ThrHisLeu	201
Db	1685	-----	-----	Db	951	GGCAGCAGCCTGAAAGAAGATGTTGCTCCCTAGAGGCCGCTCAGACAACACCTG	1010
Qy	RESULT 13	-----	-----	Qy	202	AspThrIlysProGlyTyrAsnGluIleProGluArgGluIusnGlyAsnThr	221
;	Sequence 398, Application US/10101510	-----	-----	Qy	222	IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu	241
;	Publication No. US2003014295A1	-----	-----	Db	1047	-----TTGACCAAAAGCAGCTCGACAGCTTGAACACAGCTTGAACACAGGA-----AAA	1091
;	GENERAL INFORMATION:	-----	-----	Qy	242	GlySerAsnAspIleMet-----GlySerIleAspIleAsnGlyAsnGlyAsnThr	255
;	APPLICANT: WAN, JACKSON	-----	-----	Db	1092	GGAGCAGAGACCTGTTGCCAAAGGTAAGAGAAAGGGTTCAACAACTAAAGCTCCA	1151
;	APPLICANT: WANG, YIXIN	-----	-----	Qy	256	ProlyArgGluGlyAsnArgValAspAlaGlySerGinAsnAlaHisIleGlyLysVal	275
;	FILE REFERENCE: 15117.0012	-----	-----	Db	1152	GAGGGAGACTGAAACTATTTGAGAAACTCTGGCTC--CTCCCTAAAGT	1208
;	FILE REFERENCE: 15117.0012	-----	-----	Qy	276	-----GluPhenIleTyrPro-----	280
;	CURRENT APPLICATION NUMBER: US/10/101,510	-----	-----	Db	1209	GAGGAGAGATGGAGGATGATTCAGCACCCACCATGTCCTTGAATCCTACCTC	1268
;	CURRENT FILING DATE: 2002-03-20	-----	-----	Qy	281	-----ProAlaProSerLysGluIleArgGlySerAspAlaIleGluSer 298	-----
;	PRIOR APPLICATION NUMBER: 60/1276, 947	-----	-----	Db	1269	AGCTATGCCAGGCCGAAAGAAAAGAAAAGATTGAAACT--TCAGCCACGGCA	1325
;	NUMBER OF SEQ ID NO: 805	-----	-----	Qy	299	ThrAsnTyrAsnGluIleProlyAsnClyLysGlySerIleArgGlyValAspHis	318
;	SOFTWARE: PatentIn Ver. 2.1	-----	-----	Db	1326	CTTGAGATAAAGGACTAAARAAATGACTCTTAAAGCTAAACTGGTCA	1385
;	SEQ ID NO: 398	-----	-----	Qy	319	SerAsnArgAsnGlnAlaThrIleAsnGluLysGlnArgPheProSerLysGlyLysSer	338
;	LENGTH: 4839	-----	-----	Db	1386	GTTGAGAAATTACCCAGGTGAAACAAACGAGTCAGAGAACCCGCTGAGCTGATT	1445
;	ORGANISM: Homo sapiens	-----	-----	Qy	339	GlnGlyLeu-----	341
;	FEATURE: modified_base	-----	-----	Db	1446	GCCAAAGCTGAGAAAGGTGCTGCTGATGTTGCCAGTGTGCAAGACTCCCGTTACCGCG	1505
;	NAME/KEY: modified_base	-----	-----	-----	-----	-----	-----
;	OTHER INFORMATION: a, t, c, g, other or unknown	-----	-----	-----	-----	-----	-----
;	FEATURE: modified_base	-----	-----	-----	-----	-----	-----
;	NAME/KEY: modified_base	-----	-----	-----	-----	-----	-----
;	LOCATION: (428)	-----	-----	-----	-----	-----	-----
;	OTHER INFORMATION: a, t, c, g, other or unknown	-----	-----	-----	-----	-----	-----
;	US-10-101-510-398	-----	-----	-----	-----	-----	-----
;	Alignment Scores:	-----	-----	-----	-----	-----	-----
;	Pred. No.:	0.00187	Length:	4839	-----	-----	-----
;	Score:	140.00	Matches:	87	-----	-----	-----
;	Percent Similarity:	32.08%	Conservative:	49	-----	-----	-----
;	Best Local Similarity:	20.52%	Mismatches:	144	-----	-----	-----
;	Query Match:	6.14%	Indels:	144	-----	-----	-----
;	DB:	12	Gaps:	17	-----	-----	-----
;	-----	-----	-----	-----	-----	-----	-----
;	US-09-700-696C-2 (1-430) x US-10-101-510-398 (1-4839)	-----	-----	-----	-----	-----	-----

CURRENT APPLICATION NUMBER: US/10/161,572
 CURRENT FILING DATE: 2002-06-03
 PRIOR APPLICATION NUMBER: US 60/296,076
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/328,605
 PRIOR FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: US 60/338,733
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/357,253
 PRIOR FILING DATE: 2002-02-15
 PRIOR APPLICATION NUMBER: US 60/357,600
 PRIOR FILING DATE: 2002-02-15
 NUMBER OF SEQ ID NOS: 63
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 8
 LENGTH: 16991
 TYPE: DNA
 ORGANISM: Homo sapiens
 S-11-0-161-572-8

Alignment Scores:

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Percent Local Similarity:	37.87%	Matches:	105
Best Local Similarity:	25.99%	Conservative:	48
Query Match:	6.10%	Mismatches:	162
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		Gaps:	17

US-09-700-696C-2 (1-430) x US-10-161-572-8 (1-36991)

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 881 AAACAGCGCATCCGGTAATCTAGTC---ATGAGCCAAAGCTCCAGTCCACCAA 937

b 94 AlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGlnLysSerProVal 113
 938 TCGAACAGCAAAAGGCCCTTCTAACGGCCAGGGCAGCTCCCG-AGTCGCGAG 996

b 114 LysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLysLysLeuSerLys 133
 997 CAAAGAAAGAACCCAGCCGGTAGCAC 1041

b 134 ValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeuGluArgLys 153
 1042 -----
 1059 -----
 1059 -----
 1059 -----
 1060 CGACCTGAGGCCACCGGGCACACACCGGGTAGACACCTG-GGAGAA 1118

b 174 GluGluAla-----
 1119 GGGGAGGCCAGCTCCAAGAGGTCAACCCACCCAGGCCAGACTCTT-GCCAGG---ATA 1174

b 187 GluThrGlyAlaAlaGlyProSerGluAlaGluSerThrIleAspThr-----
 1175 AGAACCTCATGGTCCAGACAGGCAAGCTGGCAAGCAGGTGAAACTCCACCTTCACAGCAA 1234

b 204 -----
 1235 AAAGGGAGCCGGGAGAGTTACGCCGOCCTAGAACCCACAACGGGAAAGGGGTGAC 1294

b 218 -----
 1295 AGCCAGCCTAGAAATCTGAGAAGAGGTACGCCACAGGGCTAGGATTAAGGG 1354

b 224 ThrArgAspGlu-----
 1355 AGGAGTCCGGCTGTAACTCCAGTAGCCAGTCAGCTCAAACCCGACTGGAAATT 1414

b 238 SerLeuValGluGlySerAspIleMetGlySerThrAsnPhyLysGlu-----
 1415 CCCTCCAAAGGAGAACGGTGCACACCCATCTCCATCTCAAGGAAAGGTGAGGCTAC 1474

Search completed: November 30, 2003, 02:24:21
 Job time : 460 secs